HUMANIZED ANTIBODIES THAT RECOGNIZE BETA AMYLOID PEPTIDE

Related Applications

This application is a continuation-in-part of prior-filed application U.S. Serial No. 10/010,942 filed December 6, 2001 entitled "Humanized Antibodies that Recognize Beta Amyloid Peptide" (pending) which, in turn, claims the benefit of prior-filed provisional patent application U.S. Serial No. 60/251,892 (filed December 6, 2000) entitled "Humanized Antibodies That Recognize Beta-Amyloid Peptide" (expired). The entire content of the above-referenced applications is incorporated herein by reference.

Background of the Invention

Alzheimer's disease (AD) is a progressive disease resulting in senile dementia. *See generally* Selkoe, *TINS* 16:403 (1993); Hardy *et al.*, WO 92/13069; Selkoe, *J. Neuropathol. Exp. Neurol.* 53:438 (1994); Duff *et al.*, *Nature* 373:476 (1995); Games *et al.*, *Nature* 373:523 (1995). Broadly speaking, the disease falls into two categories: late onset, which occurs in old age (65 + years) and early onset, which develops well before the senile period, *i.e.*, between 35 and 60 years. In both types of disease, the pathology is the same but the abnormalities tend to be more severe and widespread in cases beginning at an earlier age. The disease is characterized by at least two types of lesions in the brain, neurofibrillary tangles and senile plaques. Neurofibrillary tangles are intracellular deposits of microtubule associated tau protein consisting of two filaments twisted about each other in pairs. Senile plaques (*i.e.*, amyloid plaques) are areas of disorganized neuropil up to 150 μm across with extracellular amyloid deposits at the center which are visible by microscopic analysis of sections of brain tissue. The accumulation of amyloid plaques within the brain is also associated with Down's syndrome and other cognitive disorders.

The principal constituent of the plaques is a peptide termed Aβ or β-amyloid peptide. Aβ peptide is a 4-kDa internal fragment of 39-43 amino acids of a larger transmembrane glycoprotein named protein termed amyloid precursor protein (APP). As a result of proteolytic processing of APP by different secretase enzymes, Aβ is primarily found in both a short form, 40 amino acids in length, and a long form, ranging from 42-43 amino acids in length. Part of the hydrophobic transmembrane

domain of APP is found at the carboxy end of Aβ, and may account for the ability of Aβ to aggregate into plaques, particularly in the case of the long form. Accumulation of amyloid plaques in the brain eventually leads to neuronal cell death. The physical symptoms associated with this type of neural deterioration characterize Alzheimer's disease.

Several mutations within the APP protein have been correlated with the presence of Alzheimer's disease. See, *e.g.*, Goate *et al.*, *Nature* 349:704) (1991) (valine^{717} to isoleucine); Chartier Harlan *et al. Nature* 353:844 (1991)) (valine^{717} to glycine); Murrell *et al.*, *Science* 254:97 (1991) (valine^{717} to phenylalanine); Mullan *et al.*, *Nature Genet.* 1:345 (1992) (a double mutation changing lysine^{595}-methionine^{596} to asparagine^{595}-leucine^{596}). Such mutations are thought to cause Alzheimer's disease by increased or altered processing of APP to Aβ, particularly processing of APP to increased amounts of the long form of Aβ (*i.e.*, Aβ1-42 and Aβ1-43). Mutations in other genes, such as the presenilin genes, PS1 and PS2, are thought indirectly to affect processing of APP to generate increased amounts of long form Aβ (see Hardy, *TINS* 20: 154 (1997)).

Mouse models have been used successfully to determine the significance of amyloid plaques in Alzheimer's (Games *et al.*, *supra*, Johnson-Wood *et al.*, *Proc. Natl. Acad. Sci. USA* 94:1550 (1997)). In particular, when PDAPP transgenic mice, (which express a mutant form of human APP and develop Alzheimer's disease at a young age), are injected with the long form of Aβ, they display both a decrease in the progression of Alzheimer's and an increase in antibody titers to the Aβ peptide (Schenk *et al.*, *Nature* 400, 173 (1999)). The observations discussed above indicate that Aβ, particularly in its long form, is a causative element in Alzheimer's disease.

McMichael, EP 526,511, proposes administration of homeopathic dosages (less than or equal to 10^{-2} mg/day) of Aβ to patients with preestablished AD. In a typical human with about 5 liters of plasma, even the upper limit of this dosage would be expected to generate a concentration of no more than 2 pg/ml. The normal concentration of Aβ in human plasma is typically in the range of 50-200 pg/ml (Seubert *et al.*, *Nature* 359:325 (1992)). Because EP 526,511's proposed dosage would barely alter the level of endogenous circulating Aβ and because EP 526,511 does not

recommend use of an adjuvant, as an immunostimulant, it seems implausible that any therapeutic benefit would result.

Accordingly, there exists the need for new therapies and reagents for the treatment of Alzheimer's disease, in particular, therapies and reagents capable of effecting a therapeutic benefit at physiologic (*e.g.*, non-toxic) doses.

Summary of the Invention

The present invention features new immunological reagents, in particular, therapeutic antibody reagents for the prevention and treatment of amyloidogenic disease (*e.g.*, Alzheimer's disease). The invention is based, at least in part, on the identification and characterization of two monoclonal antibodies that specifically bind to Aβ peptide and are effective at reducing plaque burden and/or reducing the neuritic dystrophy associated with amyloidogenic disorders. Structural and functional analysis of these antibodies leads to the design of various humanized antibodies for prophylactic and/or therapeutic use. In particular, the invention features humanization of the variable regions of these antibodies and, accordingly provides for humanized immunoglobulin or antibody chains, intact humanized immunoglobulins or antibodies, and functional immunoglobulin or antibody fragments, in particular, antigen binding fragments, of the featured antibodies.

Polypeptides comprising the complementarity determining regions of the featured monoclonal antibodies are also disclosed, as are polynucleotide reagents, vectors and host suitable for encoding said polypeptides.

Methods of treatment of amyloidogenic diseases or disorders (*e.g.*, Alzheimer's disease) are disclosed, as are pharmaceutical compositions and kits for use in such applications.

Also featured are methods of identifying residues within the featured monoclonal antibodies which are important for proper immunologic function and for identifying residues which are amenable to substitution in the design of humanized antibodies having improved binding affinities and/or reduced immunogenicity, when used as therapeutic reagents.

Also featured are antibodies (*e.g.*, humanized antibodies) having altered effector functions, and therapeutic uses thereof.

Brief Description of the Drawings

Figure 1 depicts an alignment of the amino acid sequences of the light chain of mouse 3D6, humanized 3D6, Kabat ID 109230 and germline A19 antibodies. CDR regions are indicated by arrows. Bold italics indicate rare murine residues. Bold indicates packing (VH + VL) residues. Solid fill indicates canonical/CDR interacting residues. Asterisks indicate residues selected for backmutation in humanized 3D6, version 1.

Figure 2 depicts an alignment of the amino acid sequences of the heavy chain of mouse 3D6, humanized 3D6, Kabat ID 045919 and germline VH3-23 antibodies. Annotation is the same as for Figure 1.

Figure 3 graphically depicts the Aβ binding properties of 3D6, chimeric 3D6 and 10D5. *Figure 3A* is a graph depicting binding of Aβ to chimeric 3D6 (PK1614) as compared to murine 3D6. *Figure 3B* is a graph depicting competition of biotinylated 3D6 versus unlabeled 3D6, PK1614 and 10D5 for binding to Aβ.

Figure 4 depicts a homology model of 3D6 VH and VL, showing α-carbon backbone trace. VH is shown in as a stippled line, and VL is shown as a solid line. CDR regions are indicated in ribbon form.

Figure 5 graphically depicts the Aβ binding properties of chimeric 3D6 and humanized 3D6. *Figure 5A* depicts ELISA results measuring the binding of humanized 3D6v1 and chimeric 3D6 to aggregated Aβ. *Figure 5B* depicts ELISA results measuring the binding of humanized 3D6v1 and humanized 3D6v2 to aggregated Aβ.

Figure 6 is a graph quantitating the binding of humanized 3D6 and chimeric 3D6 to Aβ plaques from brain sections of PDAPP mice.

Figure 7 is a graph showing results of a competitive binding assay testing the ability of humanized 3D6 versions 1 and 2, chimeric 3D6, murine 3D6, and 10D5 to compete with murine 3D6 for binding to Aβ.

Figure 8 graphically depicts of an *ex vivo* phagocytosis assay testing the ability of humanized 3D6v2, chimeric 3D6, and human IgG to mediate the uptake of Aβ by microglial cells.

Figure 9 depicts an alignment of the10D5 VL and 3D6 VL amino acid sequences. Bold indicates residues that match 10D5 exactly.

Figure 10 depicts an alignment of the10D5 VH and 3D6 VH amino acid sequences. Bold indicates residues that match 10D5 exactly.

Detailed Description of the Invention

The present invention features new immunological reagents and methods for preventing or treating Alzheimer's disease or other amyloidogenic diseases. The invention is based, at least in part, on the characterization of two monoclonal immunoglobulins, 3D6 and 10D5, effective at binding beta amyloid protein (Aβ) (*e.g.*, binding soluble and/or aggregated Aβ), mediating phagocytosis (*e.g.*, of aggregated Aβ), reducing plaque burden and/or reducing neuritic dystrophy (*e.g.*, in patient). The invention is further based on the determination and structural characterization of the primary and secondary structure of the variable light and heavy chains of these immunoglobulins and the identification of residues important for activity and immunogenicity.

Immunoglobulins are featured which include a variable light and/or variable heavy chain of the preferred monoclonal immunoglobulins described herein. Preferred immunoglobulins, *e.g.*, therapeutic immunoglobulins, are featured which include a humanized variable light and/or humanized variable heavy chain. Preferred variable light and/or variable heavy chains include a complementarity determining region (CDR) from the monoclonal immunoglobulin (*e.g.*, donor immunoglobulin) and variable framework regions substantially from a human acceptor immunoglobulin. The phrase "substantially from a human acceptor immunoglobulin" means that the majority or key framework residues are from the human acceptor sequence, allowing however, for substitution of residues at certain positions with residues selected to improve activity of the humanized immunoglobulin (*e.g.*, alter activity such that it more closely mimics

the activity of the donor immunoglobulin) or selected to decrease the immunogenicity of the humanized immunoglobulin.

In one embodiment, the invention features a humanized immunoglobulin light or heavy chain that includes 3D6 variable region complementarity determining regions (CDRs) (*i.e.*, includes one, two or three CDRs from the light chain variable region sequence set forth as SEQ ID NO:2 or includes one, two or three CDRs from the heavy chain variable region sequence set forth as SEQ ID NO:4), and includes a variable framework region substantially from a human acceptor immunoglobulin light or heavy chain sequence, provided that at least one residue of the framework residue is backmutated to a corresponding murine residue, wherein said backmutation does not substantially affect the ability of the chain to direct Aβ binding.

In another embodiment, the invention features a humanized immunoglobulin light or heavy chain that includes 3D6 variable region complementarity determining regions (CDRs) (*e.g.*, includes one, two or three CDRs from the light chain variable region sequence set forth as SEQ ID NO:2 and/or includes one, two or three CDRs from the heavy chain variable region sequence set forth as SEQ ID NO:4), and includes a variable framework region substantially from a human acceptor immunoglobulin light or heavy chain sequence, provided that at least one framework residue is substituted with the corresponding amino acid residue from the mouse 3D6 light or heavy chain variable region sequence, where the framework residue is selected from the group consisting of (a) a residue that non-covalently binds antigen directly; (b) a residue adjacent to a CDR; (c) a CDR-interacting residue (*e.g.*, identified by modeling the light or heavy chain on the solved structure of a homologous known immunoglobulin chain); and (d) a residue participating in the VL-VH interface.

In another embodiment, the invention features a humanized immunoglobulin light or heavy chain that includes 3D6 variable region CDRs and variable framework regions from a human acceptor immunoglobulin light or heavy chain sequence, provided that at least one framework residue is substituted with the corresponding amino acid residue from the mouse 3D6 light or heavy chain variable region sequence, where the framework residue is a residue capable of affecting light chain variable region conformation or function as identified by analysis of a three-dimensional model of the variable region, for example a residue capable of interacting

with antigen, a residue proximal to the antigen binding site, a residue capable of interacting with a CDR, a residue adjacent to a CDR, a residue within 6 Å of a CDR residue, a canonical residue, a vernier zone residue, an interchain packing residue, an unusual residue, or a glycoslyation site residue on the surface of the structural model.

In another embodiment, the invention features a humanized immunoglobulin light chain that includes 3D6 variable region CDRs (*e.g.*, from the 3D6 light chain variable region sequence set forth as SEQ ID NO:2), and includes a human acceptor immunoglobulin variable framework region, provided that at least one framework residue selected from the group consisting of L1, L2, L36 and L46 (Kabat numbering convention) is substituted with the corresponding amino acid residue from the mouse 3D6 light chain variable region sequence. In another embodiment, the invention features a humanized immunoglobulin heavy chain that includes 3D6 variable region CDRs (*e.g.*, from the 3D6 heavy chain variable region sequence set forth as SEQ ID NO:4), and includes a human acceptor immunoglobulin variable framework region, provided that at least one framework residue selected from the group consisting of H49, H93 and H94 (Kabat numbering convention) is substituted with the corresponding amino acid residue from the mouse 3D6 heavy chain variable region sequence.

Preferred light chains include kappa II framework regions of the subtype kappa II (Kabat convention), for example, framework regions from the acceptor immunoglobulin Kabat ID 019230, Kabat ID 005131, Kabat ID 005058, Kabat ID 005057, Kabat ID 005059, Kabat ID U21040 and Kabat ID U41645. Preferred heavy chains include framework regions of the subtype III (Kabat convention), for example, framework regions from the acceptor immunoglobulin Kabat ID 045919, Kabat ID 000459, Kabat ID 000553, Kabat ID 000386 and Kabat ID M23691.

In one embodiment, the invention features a humanized immunoglobulin light or heavy chain that includes 10D5 variable region complementarity determining regions (CDRs) (*i.e.*, includes one, two or three CDRs from the light chain variable region sequence set forth as SEQ ID NO:14 or includes one, two or three CDRs from the heavy chain variable region sequence set forth as SEQ ID NO:16), and includes a variable framework region substantially from a human acceptor immunoglobulin light or heavy chain sequence, provided that at least one residue of the framework residue is

backmutated to a corresponding murine residue, wherein said backmutation does not substantially affect the ability of the chain to direct Aβ binding.

In another embodiment, the invention features a humanized immunoglobulin light or heavy chain that includes 10D5 variable region complementarity determining regions (CDRs) (*e.g.*, includes one, two or three CDRs from the light chain variable region sequence set forth as SEQ ID NO:14 and/or includes one, two or three CDRs from the heavy chain variable region sequence set forth as SEQ ID NO:16), and includes a variable framework region substantially from a human acceptor immunoglobulin light or heavy chain sequence, provided that at least one framework residue is substituted with the corresponding amino acid residue from the mouse 3D6 light or heavy chain variable region sequence, where the framework residue is selected from the group consisting of (a) a residue that non-covalently binds antigen directly; (b) a residue adjacent to a CDR; (c) a CDR-interacting residue (*e.g.*, identified by modeling the light or heavy chain on the solved structure of a homologous known immunoglobulin chain); and (d) a residue participating in the VL-VH interface.

In another embodiment, the invention features a humanized immunoglobulin light or heavy chain that includes 10D5 variable region CDRs and variable framework regions from a human acceptor immunoglobulin light or heavy chain sequence, provided that at least one framework residue is substituted with the corresponding amino acid residue from the mouse 10D5 light or heavy chain variable region sequence, where the framework residue is a residue capable of affecting light chain variable region conformation or function as identified by analysis of a three-dimensional model of the variable region, for example a residue capable of interacting with antigen, a residue proximal to the antigen binding site, a residue capable of interacting with a CDR, a residue adjacent to a CDR, a residue within 6 Å of a CDR residue, a canonical residue, a vernier zone residue, an interchain packing residue, an unusual residue, or a glycoslyation site residue on the surface of the structural model.

In another embodiment, the invention features, in addition to the substitutions described above, a substitution of at least one rare human framework residue. For example, a rare residue can be substituted with an amino acid residue which is common for human variable chain sequences at that position. Alternatively, a rare residue can be substituted with a corresponding amino acid residue from a

homologous germline variable chain sequence (*e.g.*, a rare light chain framework residue can be substituted with a corresponding germline residue from an A1, A17, A18, A2, or A19 germline immunoglobulin sequence or a rare heavy chain framework residue can be substituted with a corresponding germline residue from a VH3-48, VH3-23, VH3-7, VH3-21 or VH3-11 germline immunoglobulin sequence.

In another embodiment, the invention features a humanized immunoglobulin that includes a light chain and a heavy chain, as described above, or an antigen-binding fragment of said immunoglobulin. In an exemplary embodiment, the humanized immunoglobulin binds (*e.g.*, specifically binds) to beta amyloid peptide (Aβ) with a binding affinity of at least 10^7 M^{-1}, 10^8 M^{-1}, or 10^9 M^{-1}. In another embodiment, the immunoglobulin or antigen binding fragment includes a heavy chain having isotype γ1. In another embodiment, the immunoglobulin or antigen binding fragment binds (*e.g.*, specifically binds) to both soluble beta amyloid peptide (Aβ) and aggregated Aβ. In another embodiment, the immunoglobulin or antigen binding fragment mediates phagocytosis (*e.g.*, induces phagocytosis) of beta amyloid peptide (Aβ). In yet another embodiment, the immunoglobulin or antigen binding fragment crosses the blood-brain barrier in a subject. In yet another embodiment, the immunoglobulin or antigen binding fragment reduces both beta amyloid peptide (Aβ) burden and neuritic dystrophy in a subject.

In another embodiment, the invention features chimeric immunoglobulins that include 3D6 variable regions (*e.g.*, the variable region sequences set forth as SEQ ID NO:2 or SEQ ID NO:4). As used herein, an antibody or immunoglobulin sequence comprising a VL and/or VH sequence as set forth in, for example, SEQ ID NO:2 or SEQ ID NO:4 can comprise either the full VL or VH sequence or can comprise the mature VL or VH sequence (*i.e.*, mature peptide without the signal or leader peptide). In yet another embodiment, the invention features an immunoglobulin, or antigen-binding fragment thereof, including a variable heavy chain region as set forth in SEQ ID NO:8 and a variable light chain region as set forth in SEQ ID NO:5. In yet another embodiment, the invention features an immunoglobulin, or antigen-binding fragment thereof, including a variable heavy chain region as set forth in SEQ ID NO:12 and a variable light chain region as set forth in SEQ ID NO:11. In another embodiment, the invention features chimeric immunoglobulins that include 10D5 variable regions (*e.g.*,

the variable region sequences set forth as SEQ ID NO:14 or SEQ ID NO:16). In yet another embodiment, the immunoglobulin, or antigen-binding fragment thereof, further includes constant regions from IgG1.

The immunoglobulins described herein are particularly suited for use in therapeutic methods aimed at preventing or treating amyloidogenic diseases. In one embodiment, the invention features a method of preventing or treating an amyloidogenic disease (*e.g.*, Alzheimer's disease) that involves administering to the patient an effective dosage of a humanized immunoglobulin as described herein. In another embodiment, the invention features pharmaceutical compositions that include a humanized immunoglobulin as described herein and a pharmaceutical carrier. Also featured are isolated nucleic acid molecules, vectors and host cells for producing the immunoglobulins or immunoglobulin fragments or chains described herein, as well as methods for producing said immunoglobulins, immunoglobulin fragments or immunoglobulin chains

The present invention further features a method for identifying 3D6 or 10D5 residues amenable to substitution when producing a humanized 3D6 or 10D5 immunoglobulin, respectively. For example, a method for identifying variable framework region residues amenable to substitution involves modeling the three-dimensional structure of the 3D6 or 10D5 variable region on a solved homologous immunoglobulin structure and analyzing said model for residues capable of affecting 3D6 or 10D5 immunoglobulin variable region conformation or function, such that residues amenable to substitution are identified. The invention further features use of the variable region sequence set forth as SEQ ID NO:2 or SEQ ID NO:4, or any portion thereof, in producing a three-dimensional image of a 3D6 immunoglobulin, 3D6 immunoglobulin chain, or domain thereof. Also featured is the use of the variable region sequence set forth as SEQ ID NO:14 or SEQ ID NO:16, or any portion thereof, in producing a three-dimensional image of a 10D5 immunoglobulin, 10D5 immunoglobulin chain, or domain thereof.

The present invention further features immunoglobulins having altered effector function, such as the ability to bind effector molecules, for example, complement or a receptor on an effector cell. In particular, the immunoglobulin of the invention has an altered constant region, *e.g.*, Fc region, wherein at least one amino acid

residue in the Fc region has been replaced with a different residue or side chain. In one embodiment, the modified immunoglobulin is of the IgG class, comprises at least one amino acid residue replacement in the Fc region such that the immunoglobulin has an altered effector function, *e.g.*, as compared with an unmodified immunoglobulin. In particular embodiments, the immunoglobulin of the invention has an altered effector function such that it is less immunogenic (*e.g.*, does not provoke undesired effector cell activity, lysis, or complement binding), has improved amyloid clearance properties, and/or has a desirable half-life.

Prior to describing the invention, it may be helpful to an understanding thereof to set forth definitions of certain terms to be used hereinafter.

The term “immunoglobulin” or “antibody” (used interchangeably herein) refers to an antigen-binding protein having a basic four-polypeptide chain structure consisting of two heavy and two light chains, said chains being stabilized, for example, by interchain disulfide bonds, which has the ability to specifically bind antigen. Both heavy and light chains are folded into domains. The term “domain” refers to a globular region of a heavy or light chain polypeptide comprising peptide loops (*e.g.*, comprising 3 to 4 peptide loops) stabilized, for example, by β-pleated sheet and/or intrachain disulfide bond. Domains are further referred to herein as “constant” or “variable”, based on the relative lack of sequence variation within the domains of various class members in the case of a “constant” domain, or the significant variation within the domains of various class members in the case of a “variable” domain. “Constant” domains on the light chain are referred to interchangeably as “light chain constant regions”, “light chain constant domains”, “CL” regions or “CL” domains). “Constant” domains on the heavy chain are referred to interchangeably as “heavy chain constant regions”, “heavy chain constant domains”, “CH” regions or “CH” domains). “Variable” domains on the light chain are referred to interchangeably as “light chain variable regions”, “light chain variable domains”, “VL” regions or “VL” domains). “Variable” domains on the heavy chain are referred to interchangeably as “heavy chain constant regions”, “heavy chain constant domains”, “CH” regions or “CH” domains).

The term “region” refers to a part or portion of an antibody chain and includes constant or variable domains as defined herein, as well as more discrete parts or

portions of said domains. For example, light chain variable domains or regions include "complementarity determining regions" or "CDRs" interspersed among "framework regions" or "FRs", as defined herein.

Immunoglobulins or antibodies can exist in monomeric or polymeric form. The term "antigen-binding fragment" refers to a polypeptide fragment of an immunoglobulin or antibody binds antigen or competes with intact antibody (*i.e.*, with the intact antibody from which they were derived) for antigen binding (*i.e.*, specific binding). The term "conformation" refers to the tertiary structure of a protein or polypeptide (*e.g.*, an antibody, antibody chain, domain or region thereof). For example, the phrase "light (or heavy) chain conformation" refers to the tertiary structure of a light (or heavy) chain variable region, and the phrase "antibody conformation" or "antibody fragment conformation" refers to the tertiary structure of an antibody or fragment thereof.

"Specific binding" of an antibody mean that the antibody exhibits appreciable affinity for antigen or a preferred epitope and, preferably, does not exhibit significant crossreactivity. "Appreciable" or preferred binding include binding with an affinity of at least 10^6, 10^7, 10^8, 10^9 M^{-1}, or 10^{10} M^{-1}. Affinities greater than 10^7 M^{-1}, preferably greater than 10^8 M^{-1} are more preferred. Values intermediate of those set forth herein are also intended to be within the scope of the present invention and a preferred binding affinity can be indicated as a range of affinities, for example, 10^6 to 10^{10} M^{-1}, preferably 10^7 to 10^{10} M^{-1}, more preferably 10^8 to 10^{10} M^{-1}. An antibody that "does not exhibit significant crossreactivity" is one that will not appreciably bind to an undesirable entity (*e.g.*, an undesirable proteinaceous entity). For example, an antibody that specifically binds to Aβ will appreciably bind Aβ but will not significantly react with non-Aβ proteins or peptides (*e.g.*, non-Aβ proteins or peptides included in plaques). An antibody specific for a preferred epitope will, for example, not significantly crossreact with remote epitopes on the same protein or peptide. Specific binding can be determined according to any art-recognized means for determining such binding. Preferably, specific binding is determined according to Scatchard analysis and/or competitive binding assays.

Binding fragments are produced by recombinant DNA techniques, or by enzymatic or chemical cleavage of intact immunoglobulins. Binding fragments include

Fab, Fab', $F(ab')_2$, Fabc, Fv, single chains, and single-chain antibodies. Other than "bispecific" or "bifunctional" immunoglobulins or antibodies, an immunoglobulin or antibody is understood to have each of its binding sites identical. A "bispecific" or "bifunctional antibody" is an artificial hybrid antibody having two different heavy/light chain pairs and two different binding sites. Bispecific antibodies can be produced by a variety of methods including fusion of hybridomas or linking of Fab' fragments. See, *e.g.*, Songsivilai & Lachmann, *Clin. Exp. Immunol.* 79:315-321 (1990); Kostelny *et al.*, *J. Immunol.* 148, 1547-1553 (1992).

The term "humanized immunoglobulin" or "humanized antibody" refers to an immunoglobulin or antibody that includes at least one humanized immunoglobulin or antibody chain (*i.e.*, at least one humanized light or heavy chain). The term "humanized immunoglobulin chain" or "humanized antibody chain" (*i.e.*, a "humanized immunoglobulin light chain" or "humanized immunoglobulin heavy chain") refers to an immunoglobulin or antibody chain (*i.e.*, a light or heavy chain, respectively) having a variable region that includes a variable framework region substantially from a human immunoglobulin or antibody and complementarity determining regions (CDRs) (*e.g.*, at least one CDR, preferably two CDRs, more preferably three CDRs) substantially from a non-human immunoglobulin or antibody, and further includes constant regions (*e.g.*, at least one constant region or portion thereof, in the case of a light chain, and preferably three constant regions in the case of a heavy chain). The term "humanized variable region" (*e.g.*, "humanized light chain variable region" or "humanized heavy chain variable region") refers to a variable region that includes a variable framework region substantially from a human immunoglobulin or antibody and complementarity determining regions (CDRs) substantially from a non-human immunoglobulin or antibody.

The phrase "substantially from a human immunoglobulin or antibody" or "substantially human" means that, when aligned to a human immunoglobulin or antibody amino sequence for comparison purposes, the region shares at least 80-90%, preferably 90-95%, more preferably 95-99% identity (*i.e.*, local sequence identity) with the human framework or constant region sequence, allowing, for example, for conservative substitutions, consensus sequence substitutions, germline substitutions, backmutations, and the like. The introduction of conservative substitutions, consensus

sequence substitutions, germline substitutions, backmutations, and the like, is often referred to as "optimization" of a humanized antibody or chain. The phrase "substantially from a non-human immunoglobulin or antibody" or "substantially non-human" means having an immunoglobulin or antibody sequence at least 80-95%, preferably 90-95%, more preferably, 96%, 97%, 98%, or 99% identical to that of a non-human organism, *e.g.*, a non-human mammal.

Accordingly, all regions or residues of a humanized immunoglobulin or antibody, or of a humanized immunoglobulin or antibody chain, except possibly the CDRs, are substantially identical to the corresponding regions or residues of one or more native human immunoglobulin sequences. The term "corresponding region" or "corresponding residue" refers to a region or residue on a second amino acid or nucleotide sequence which occupies the same (*i.e.*, equivalent) position as a region or residue on a first amino acid or nucleotide sequence, when the first and second sequences are optimally aligned for comparison purposes.

The terms "humanized immunoglobulin" or "humanized antibody" are not intended to encompass chimeric immunoglobulins or antibodies, as defined *infra*. Although humanized immunoglobulins or antibodies are chimeric in their construction (*i.e.*, comprise regions from more than one species of protein), they include additional features (*i.e.*, variable regions comprising donor CDR residues and acceptor framework residues) not found in chimeric immunoglobulins or antibodies, as defined herein.

The term "significant identity" means that two polypeptide sequences, when optimally aligned, such as by the programs GAP or BESTFIT using default gap weights, share at least 50-60% sequence identity, preferably 60-70% sequence identity, more preferably 70-80% sequence identity, more preferably at least 80-90% identity, even more preferably at least 90-95% identity, and even more preferably at least 95% sequence identity or more (*e.g.*, 99% sequence identity or more). The term "substantial identity" means that two polypeptide sequences, when optimally aligned, such as by the programs GAP or BESTFIT using default gap weights, share at least 80-90% sequence identity, preferably 90-95% sequence identity, and more preferably at least 95% sequence identity or more (*e.g.*, 99% sequence identity or more). For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and

reference sequences are input into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. The sequence comparison algorithm then calculates the percent sequence identity for the test sequence(s) relative to the reference sequence, based on the designated program parameters. The terms "sequence identity" and "sequence identity" are used interchangeably herein.

Optimal alignment of sequences for comparison can be conducted, *e.g.*, by the local homology algorithm of Smith & Waterman, *Adv. Appl. Math.* 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, *J. Mol. Biol.* 48:443 (1970), by the search for similarity method of Pearson & Lipman, *Proc. Nat'l. Acad. Sci. USA* 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by visual inspection (*see generally* Ausubel *et al.,* Current Protocols in Molecular Biology). One example of algorithm that is suitable for determining percent sequence identity and sequence similarity is the BLAST algorithm, which is described in Altschul *et al., J. Mol. Biol.* 215:403 (1990). Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (publicly accessible through the National Institutes of Health NCBI internet server). Typically, default program parameters can be used to perform the sequence comparison, although customized parameters can also be used. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (*see* Henikoff & Henikoff, *Proc. Natl. Acad. Sci. USA* 89:10915 (1989)).

Preferably, residue positions which are not identical differ by conservative amino acid substitutions. For purposes of classifying amino acids substitutions as conservative or nonconservative, amino acids are grouped as follows: Group I (hydrophobic sidechains): leu, met, ala, val, leu, ile; Group II (neutral hydrophilic side chains): cys, ser, thr; Group III (acidic side chains): asp, glu; Group IV (basic side chains): asn, gln, his, lys, arg; Group V (residues influencing chain orientation): gly, pro; and Group VI (aromatic side chains): trp, tyr, phe. Conservative substitutions involve substitutions between amino acids in the same class. Non-

conservative substitutions constitute exchanging a member of one of these classes for a member of another.

Preferably, humanized immunoglobulins or antibodies bind antigen with an affinity that is within a factor of three, four, or five of that of the corresponding non-human antibody. For example, if the nonhuman antibody has a binding affinity of 10^9 M^{-1}, humanized antibodies will have a binding affinity of at least 3×10^9 M^{-1}, 4×10^9 M^{-1} or 10^9 M^{-1}. When describing the binding properties of an immunoglobulin or antibody chain, the chain can be described based on its ability to "direct antigen (*e.g.*, Aβ) binding". A chain is said to "direct antigen binding" when it confers upon an intact immunoglobulin or antibody (or antigen binding fragment thereof) a specific binding property or binding affinity. A mutation (*e.g.*, a backmutation) is said to substantially affect the ability of a heavy or light chain to direct antigen binding if it affects (*e.g.*, decreases) the binding affinity of an intact immunoglobulin or antibody (or antigen binding fragment thereof) comprising said chain by at least an order of magnitude compared to that of the antibody (or antigen binding fragment thereof) comprising an equivalent chain lacking said mutation. A mutation "does not substantially affect (*e.g.*, decrease) the ability of a chain to direct antigen binding" if it affects (*e.g.*, decreases) the binding affinity of an intact immunoglobulin or antibody (or antigen binding fragment thereof) comprising said chain by only a factor of two, three, or four of that of the antibody (or antigen binding fragment thereof) comprising an equivalent chain lacking said mutation.

The term "chimeric immunoglobulin" or antibody refers to an immunoglobulin or antibody whose variable regions derive from a first species and whose constant regions derive from a second species. Chimeric immunoglobulins or antibodies can be constructed, for example by genetic engineering, from immunoglobulin gene segments belonging to different species.

An "antigen" is an entity (*e.g.*, a protenaceous entity or peptide) to which an antibody specifically binds.

The term "epitope" or "antigenic determinant" refers to a site on an antigen to which an immunoglobulin or antibody (or antigen binding fragment thereof) specifically binds. Epitopes can be formed both from contiguous amino acids or noncontiguous amino acids juxtaposed by tertiary folding of a protein. Epitopes formed

from contiguous amino acids are typically retained on exposure to denaturing solvents whereas epitopes formed by tertiary folding are typically lost on treatment with denaturing solvents. An epitope typically includes at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 or 15 amino acids in a unique spatial conformation. Methods of determining spatial conformation of epitopes include, for example, x-ray crystallography and 2-dimensional nuclear magnetic resonance. See, *e.g.*, *Epitope Mapping Protocols in Methods in Molecular Biology,* Vol. 66, G. E. Morris, Ed. (1996).

Antibodies that recognize the same epitope can be identified in a simple immunoassay showing the ability of one antibody to block the binding of another antibody to a target antigen, *i.e.*, a competitive binding assay. Competitive binding is determined in an assay in which the immunoglobulin under test inhibits specific binding of a reference antibody to a common antigen, such as Aβ. Numerous types of competitive binding assays are known, for example: solid phase direct or indirect radioimmunoassay (RIA), solid phase direct or indirect enzyme immunoassay (EIA), sandwich competition assay (see Stahli *et al.*, *Methods in Enzymology* 9:242 (1983)); solid phase direct biotin-avidin EIA (see Kirkland *et al.*, *J. Immunol.* 137:3614 (1986)); solid phase direct labeled assay, solid phase direct labeled sandwich assay (see Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Press (1988)); solid phase direct label RIA using I-125 label (see Morel *et al.*, *Mol. Immunol.* 25(1):7 (1988)); solid phase direct biotin-avidin EIA (Cheung *et al.*, *Virology* 176:546 (1990)); and direct labeled RIA. (Moldenhauer *et al.*, *Scand. J. Immunol.* 32:77 (1990)). Typically, such an assay involves the use of purified antigen bound to a solid surface or cells bearing either of these, an unlabeled test immunoglobulin and a labeled reference immunoglobulin. Competitive inhibition is measured by determining the amount of label bound to the solid surface or cells in the presence of the test immunoglobulin. Usually the test immunoglobulin is present in excess. Usually, when a competing antibody is present in excess, it will inhibit specific binding of a reference antibody to a common antigen by at least 50-55%, 55-60%, 60-65%, 65-70% 70-75% or more.

An epitope is also recognized by immunologic cells, for example, B cells and/or T cells. Cellular recognition of an epitope can be determined by *in vitro* assays that measure antigen-dependent proliferation, as determined by ^{3}H-thymidine

incorporation, by cytokine secretion, by antibody secretion, or by antigen-dependent killing (cytotoxic T lymphocyte assay).

Exemplary epitopes or antigenic determinants can be found within the human amyloid precursor protein (APP), but are preferably found within the Aβ peptide of APP. Multiple isoforms of APP exist, for example APP^{695} APP^{751} and APP^{770}. Amino acids within APP are assigned numbers according to the sequence of the APP^{770} isoform (see *e.g.*, GenBank Accession No. P05067, also set forth as SEQ ID NO:38). Aβ (also referred to herein as beta amyloid peptide and A-beta) peptide is a ~4-kDa internal fragment of 39-43 amino acids of APP (Aβ39, Aβ40, Aβ41, Aβ42 and Aβ43). Aβ40, for example, consists of residues 672-711 of APP and Aβ42 consists of residues 673-713 of APP. As a result of proteolytic processing of APP by different secretase enzymes *iv vivo* or *in situ,* Aβ is found in both a "short form", 40 amino acids in length, and a "long form", ranging from 42-43 amino acids in length. Preferred epitopes or antigenic determinants, as described herein, are located within the N-terminus of the Aβ peptide and include residues within amino acids 1-10 of Aβ, preferably from residues 1-3, 1-4, 1-5, 1-6, 1-7 or 3-7 of Aβ42. Additional referred epitopes or antigenic determinants include residues 2-4, 5, 6, 7 or 8 of Aβ, residues 3-5, 6, 7, 8 or 9 of Aβ, or residues 4-7, 8, 9 or 10 of Aβ42.

The term "amyloidogenic disease" includes any disease associated with (or caused by) the formation or deposition of insoluble amyloid fibrils. Exemplary amyloidogenic diseases include, but are not limited to systemic amyloidosis, Alzheimer's disease, mature onset diabetes, Parkinson's disease, Huntington's disease, fronto-temporal dementia, and the prion-related transmissible spongiform encephalopathies (kuru and Creutzfeldt-Jacob disease in humans and scrapie and BSE in sheep and cattle, respectively). Different amyloidogenic diseases are defined or characterized by the nature of the polypeptide component of the fibrils deposited. For example, in subjects or patients having Alzheimer's disease, β-amyloid protein (*e.g.*, wild-type, variant, or truncated β-amyloid protein) is the characterizing polypeptide component of the amyloid deposit. Accordingly, Alzheimer's disease is an example of a "disease characterized by deposits of Aβ" or a "disease associated with deposits of Aβ",

e.g., in the brain of a subject or patient. The terms "β-amyloid protein", "β-amyloid peptide", "β-amyloid", "Aβ" and "Aβ peptide" are used interchangeably herein.

The term "effective dose" or "effective dosage" is defined as an amount sufficient to achieve or at least partially achieve the desired effect. The term "therapeutically effective dose" is defined as an amount sufficient to cure or at least partially arrest the disease and its complications in a patient already suffering from the disease. Amounts effective for this use will depend upon the severity of the infection and the general state of the patient's own immune system.

The term "patient" includes human and other mammalian subjects that receive either prophylactic or therapeutic treatment.

"Soluble" or "dissociated" Aβ refers to non-aggregating or disaggregated Aβ polypeptide. "Insoluble" Aβ refers to aggregating Aβ polypeptide, for example, Aβ held together by noncovalent bonds. Aβ (*e.g.*, Aβ42) is believed to aggregate, at least in part, due to the presence of hydrophobic residues at the C-terminus of the peptide (part of the transmembrane dómain of APP). One method to prepare soluble Aβ is to dissolve lyophilized peptide in neat DMSO with sonication. The resulting solution is centrifuged to remove any insoluble particulates.

The term "effector function" refers to an activity that resides in the Fc region of an antibody (*e.g.*, an IgG antibody) and includes, for example, the ability of the antibody to bind effector molecules such as complement and/or Fc receptors, which can control several immune functions of the antibody such as effector cell activity, lysis, complement-mediated activity, antibody clearance, and antibody half-life.

The term "effector molecule" refers to a molecule that is capable of binding to the Fc region of an antibody (*e.g.*, an IgG antibody) including, but not limited to, a complement protein or a Fc receptor.

The term "effector cell" refers to a cell capable of binding to the Fc portion of an antibody (*e.g.*, an IgG antibody) typically *via* an Fc receptor expressed on the surface of the effector cell including, but not limited to, lymphocytes, *e.g.*, antigen presenting cells and T cells.

The term "Fc region" refers to a C-terminal region of an IgG antibody, in particular, the C-terminal region of the heavy chain(s) of said IgG antibody. Although the boundaries of the Fc region of an IgG heavy chain can vary slightly, a Fc region is

typically defined as spanning from about amino acid residue Cys226 to the carboxyl-terminus of an IGg heavy chain(s).

The term "Kabat numbering" unless otherwise stated, is defined as the numbering of the residues in, *e.g.*, an IgG heavy chain antibody using the EU index as in Kabat *et al.* (Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, Md. (1991)), expressly incorporated herein by reference.

The term "Fc receptor" or "FcR" refers to a receptor that binds to the Fc region of an antibody. Typical Fc receptors which bind to an Fc region of an antibody (*e.g.*, an IgG antibody) include, but are not limited to, receptors of the FcγRI, FcγRII, and FcγRIII subclasses, including allelic variants and alternatively spliced forms of these receptors. Fc receptors are reviewed in Ravetch and Kinet, Annu. Rev. Immunol 9:457-92 (1991); Capel *et al.*, Immunomethods 4:25-34 (1994); and de Haas *et al.*, J. Lab. Clin. Med. 126:330-41 (1995).

I. Immunological and Therapeutic Reagents

Immunological and therapeutic reagents of the invention comprise or consist of immunogens or antibodies, or functional or antigen binding fragments thereof, as defined herein. The basic antibody structural unit is known to comprise a tetramer of subunits. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kDa) and one "heavy" chain (about 50-70 kDa). The amino-terminal portion of each chain includes a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The carboxy-terminal portion of each chain defines a constant region primarily responsible for effector function.

Light chains are classified as either kappa or lambda and are about 230 residues in length. Heavy chains are classified as gamma (γ), mu (μ), alpha (α), delta (δ), or epsilon (ε), are about 450-600 residues in length, and define the antibody's isotype as IgG, IgM, IgA, IgD and IgE, respectively. Both heavy and light chains are folded into domains. The term "domain" refers to a globular region of a protein, for example, an immunoglobulin or antibody. Immunoglobulin or antibody domains include, for example, 3 or four peptide loops stabilized by β-pleated sheet and an

interchain disulfide bond. Intact light chains have, for example, two domains (V_L and C_L) and intact heavy chains have, for example, four or five domains (V_H, C_H1, C_H2, and C_H3).

Within light and heavy chains, the variable and constant regions are joined by a "J" region of about 12 or more amino acids, with the heavy chain also including a "D" region of about 10 more amino acids. (*See generally, Fundamental Immunology* (Paul, W., ed., 2nd ed. Raven Press, N.Y. (1989), Ch. 7, incorporated by reference in its entirety for all purposes).

The variable regions of each light/heavy chain pair form the antibody binding site. Thus, an intact antibody has two binding sites. Except in bifunctional or bispecific antibodies, the two binding sites are the same. The chains all exhibit the same general structure of relatively conserved framework regions (FR) joined by three hypervariable regions, also called complementarity determining regions or CDRs. Naturally-occurring chains or recombinantly produced chains can be expressed with a leader sequence which is removed during cellular processing to produce a mature chain. Mature chains can also be recombinantly produced having a non-naturally occurring leader sequence, for example, to enhance secretion or alter the processing of a particular chain of interest.

The CDRs of the two mature chains of each pair are aligned by the framework regions, enabling binding to a specific epitope. From N-terminal to C-terminal, both light and heavy chains comprise the domains FR1, CDR1, FR2, CDR2, FR3, CDR3 and FR4. "FR4" also is referred to in the art as the D/J region of the variable heavy chain and the J region of the variable light chain. The assignment of amino acids to each domain is in accordance with the definitions of Kabat, *Sequences of Proteins of Immunological Interest* (National Institutes of Health, Bethesda, MD, 1987 and 1991). An alternative structural definition has been proposed by Chothia *et al.*, *J. Mol. Biol.* 196:901 (1987); *Nature* 342:878 (1989); and *J. Mol. Biol.* 186:651 (1989) (hereinafter collectively referred to as "Chothia *et al.*" and incorporated by reference in their entirety for all purposes).

A. Aβ Antibodies

Therapeutic agents of the invention include antibodies that specifically bind to Aβ or other component of amyloid plaques. Such antibodies can be monoclonal or polyclonal. Some such antibodies bind specifically to the aggregated form of Aβ without binding to the soluble form. Some bind specifically to the soluble form without binding to the aggregated form. Some bind to both aggregated and soluble forms. Some such antibodies bind to a naturally occurring short form of Aβ (*i.e.*, Aβ39, 40 or 41) without binding to a naturally occurring long form of Aβ (*i.e.*, Aβ42 and Aβ43). Some antibodies bind to a long form of Aβ without binding to a short form. Some antibodies bind to Aβ without binding to full-length amyloid precursor protein. Antibodies used in therapeutic methods preferably have an intact constant region or at least sufficient of the constant region to interact with an Fc receptor. Human isotype IgG1 is preferred because of it having highest affinity of human isotypes for the FcRI receptor on phagocytic cells. Bispecific Fab fragments can also be used, in which one arm of the antibody has specificity for Aβ, and the other for an Fc receptor. Preferred antibodies bind to Aβ with a binding affinity greater than (or equal to) about 10^6, 10^7, 10^8, 10^9, or 10^{10} M^{-1} (including affinities intermediate of these values).

Polyclonal sera typically contain mixed populations of antibodies binding to several epitopes along the length of Aβ. However, polyclonal sera can be specific to a particular segment of Aβ, such as Aβ1-10. Monoclonal antibodies bind to a specific epitope within Aβ that can be a conformational or nonconformational epitope. Prophylactic and therapeutic efficacy of antibodies can be tested using the transgenic animal model procedures described in the Examples. Preferred monoclonal antibodies bind to an epitope within residues 1-10 of Aβ (with the first N terminal residue of natural Aβ designated 1). Some preferred monoclonal antibodies bind to an epitope within amino acids 1-5, and some to an epitope within 5-10. Some preferred antibodies bind to epitopes within amino acids 1-3, 1-4, 1-5, 1-6, 1-7 or 3-7. Some preferred antibodies bind to an epitope starting at resides 1-3 and ending at residues 7-11 of Aβ. Less preferred antibodies include those binding to epitopes with residues 10-15, 15-20, 25-30, 10-20, 20, 30, or 10-25 of Aβ. It is recommended that such antibodies be

screened for activity in the mouse models described in the Examples before use. For example, it has been found that certain antibodies to epitopes within residues 10-18, 16-24, 18-21 and 33-42 lack activity (*e.g.*, lack the ability to reduce plaque burden and/or resolve the neuritic pathology associated with Alzheimer's disease). In some methods, multiple monoclonal antibodies having binding specificities to different epitopes are used. Such antibodies can be administered sequentially or simultaneously. Antibodies to amyloid components other than Aβ can also be used (*e.g.*, administered or co-administered). For example, antibodies can be directed to the amyloid associated protein synuclein.

When an antibody is said to bind to an epitope within specified residues, such as Aβ 1-5 for example, what is meant is that the antibody specifically binds to a polypeptide containing the specified residues (*i.e.*, Aβ 1-5 in this an example). Such an antibody does not necessarily contact every residue within Aβ 1-5. Nor does every single amino acid substitution or deletion with in Aβ1-5 necessarily significantly affect binding affinity. Epitope specificity of an antibody can be determined, for example, by forming a phage display library in which different members display different subsequences of Aβ. The phage display library is then selected for members specifically binding to an antibody under test. A family of sequences is isolated. Typically, such a family contains a common core sequence, and varying lengths of flanking sequences in different members. The shortest core sequence showing specific binding to the antibody defines the epitope bound by the antibody. Antibodies can also be tested for epitope specificity in a competition assay with an antibody whose epitope specificity has already been determined. For example, antibodies that compete with the 3D6 antibody for binding to Aβ bind to the same or similar epitope as 3D6, *i.e.*, within residues Aβ 1-5. Likewise antibodies that compete with the 10D5 antibody bind to the same or similar epitope, *i.e.*, within residues Aβ 3-7. Screening antibodies for epitope specificity is a useful predictor of therapeutic efficacy. For example, an antibody determined to bind to an epitope within residues 1-7 of Aβ is likely to be effective in preventing and treating Alzheimer's disease according to the methodologies of the present invention.

Monoclonal or polyclonal antibodies that specifically bind to a preferred segment of Aβ without binding to other regions of Aβ have a number of advantages relative to monoclonal antibodies binding to other regions or polyclonal sera to intact

Aβ. First, for equal mass dosages, dosages of antibodies that specifically bind to preferred segments contain a higher molar dosage of antibodies effective in clearing amyloid plaques. Second, antibodies specifically binding to preferred segments can induce a clearing response against amyloid deposits without inducing a clearing response against intact APP polypeptide, thereby reducing the potential side effects.

1. Production of Nonhuman Antibodies

The present invention features non-human antibodies, for example, antibodies having specificity for the preferred Aβ epitopes of the invention. Such antibodies can be used in formulating various therapeutic compositions of the invention or, preferably, provide complementarity determining regions for the production of humanized or chimeric antibodies (described in detail below). The production of non-human monoclonal antibodies, *e.g.*, murine, guinea pig, primate, rabbit or rat, can be accomplished by, for example, immunizing the animal with Aβ. A longer polypeptide comprising Aβ or an immunogenic fragment of Aβ or anti-idiotypic antibodies to an antibody to Aβ can also be used. See Harlow & Lane, *supra,* incorporated by reference for all purposes). Such an immunogen can be obtained from a natural source, by peptide synthesis or by recombinant expression. Optionally, the immunogen can be administered fused or otherwise complexed with a carrier protein, as described below. Optionally, the immunogen can be administered with an adjuvant. The term "adjuvant" refers to a compound that when administered in conjunction with an antigen augments the immune response to the antigen, but when administered alone does not generate an immune response to the antigen. Adjuvants can augment an immune response by several mechanisms including lymphocyte recruitment, stimulation of B and/or T cells, and stimulation of macrophages. Several types of adjuvant can be used as described below. Complete Freund's adjuvant followed by incomplete adjuvant is preferred for immunization of laboratory animals.

Rabbits or guinea pigs are typically used for making polyclonal antibodies. Exemplary preparation of polyclonal antibodies, *e.g.*, for passive protection, can be performed as follows. 125 non-transgenic mice are immunized with 100 μg Aβ1-42, plus CFA/IFA adjuvant, and euthanized at 4-5 months. Blood is collected from immunized mice. IgG is separated from other blood components. Antibody specific for

the immunogen may be partially purified by affinity chromatography. An average of about 0.5-1 mg of immunogen-specific antibody is obtained per mouse, giving a total of 60-120 mg.

Mice are typically used for making monoclonal antibodies. Monoclonals can be prepared against a fragment by injecting the fragment or longer form of Aβ into a mouse, preparing hybridomas and screening the hybridomas for an antibody that specifically binds to Aβ. Optionally, antibodies are screened for binding to a specific region or desired fragment of Aβ without binding to other nonoverlapping fragments of Aβ. The latter screening can be accomplished by determining binding of an antibody to a collection of deletion mutants of an Aβ peptide and determining which deletion mutants bind to the antibody. Binding can be assessed, for example, by Western blot or ELISA. The smallest fragment to show specific binding to the antibody defines the epitope of the antibody. Alternatively, epitope specificity can be determined by a competition assay is which a test and reference antibody compete for binding to Aβ. If the test and reference antibodies compete, then they bind to the same epitope or epitopes sufficiently proximal such that binding of one antibody interferes with binding of the other. The preferred isotype for such antibodies is mouse isotype IgG2a or equivalent isotype in other species. Mouse isotype IgG2a is the equivalent of human isotype IgG1.

<u>*2. Chimeric and Humanized Antibodies*</u>

The present invention also features chimeric and/or humanized antibodies (*i.e.*, chimeric and/or humanized immunoglobulins) specific for beta amyloid peptide. Chimeric and/or humanized antibodies have the same or similar binding specificity and affinity as a mouse or other nonhuman antibody that provides the starting material for construction of a chimeric or humanized antibody.

<u>A. Production of Chimeric Antibodies</u>

The term "chimeric antibody" refers to an antibody whose light and heavy chain genes have been constructed, typically by genetic engineering, from immunoglobulin gene segments belonging to different species. For example, the variable (V) segments of the genes from a mouse monoclonal antibody may be joined to human constant (C) segments, such as IgG1 and IgG4. Human isotype IgG1 is

preferred. A typical chimeric antibody is thus a hybrid protein consisting of the V or antigen-binding domain from a mouse antibody and the C or effector domain from a human antibody.

B. Production of Humanized Antibodies

The term "humanized antibody" refers to an antibody comprising at least one chain comprising variable region framework residues substantially from a human antibody chain (referred to as the acceptor immunoglobulin or antibody) and at least one complementarity determining region substantially from a mouse-antibody, (referred to as the donor immunoglobulin or antibody). See, Queen *et al.*, *Proc. Natl. Acad. Sci. USA* 86:10029-10033 (1989), US 5,530,101, US 5,585,089, US 5,693,761, US 5,693,762, Selick *et al.*, WO 90/07861, and Winter, US 5,225,539 (incorporated by reference in their entirety for all purposes). The constant region(s), if present, are also substantially or entirely from a human immunoglobulin.

The substitution of mouse CDRs into a human variable domain framework is most likely to result in retention of their correct spatial orientation if the human variable domain framework adopts the same or similar conformation to the mouse variable framework from which the CDRs originated. This is achieved by obtaining the human variable domains from human antibodies whose framework sequences exhibit a high degree of sequence identity with the murine variable framework domains from which the CDRs were derived. The heavy and light chain variable framework regions can be derived from the same or different human antibody sequences. The human antibody sequences can be the sequences of naturally occurring human antibodies or can be consensus sequences of several human antibodies. See Kettleborough *et al.*, *Protein Engineering* 4:773 (1991); Kolbinger *et al.*, *Protein Engineering* 6:971 (1993) and Carter *et al.*, WO 92/22653.

Having identified the complementarity determining regions of the murine donor immunoglobulin and appropriate human acceptor immunoglobulins, the next step is to determine which, if any, residues from these components should be substituted to optimize the properties of the resulting humanized antibody. In general, substitution of human amino acid residues with murine should be minimized, because introduction of murine residues increases the risk of the antibody eliciting a human-anti-mouse-antibody

(HAMA) response in humans. Art-recognized methods of determining immune response can be performed to monitor a HAMA response in a particular patient or during clinical trials. Patients administered humanized antibodies can be given an immunogenicity assessment at the beginning and throughout the administration of said therapy. The HAMA response is measured, for example, by detecting antibodies to the humanized therapeutic reagent, in serum samples from the patient using a method known to one in the art, including surface plasmon resonance technology (BIACORE) and/or solid-phase ELISA analysis.

Certain amino acids from the human variable region framework residues are selected for substitution based on their possible influence on CDR conformation and/or binding to antigen. The unnatural juxtaposition of murine CDR regions with human variable framework region can result in unnatural conformational restraints, which, unless corrected by substitution of certain amino acid residues, lead to loss of binding affinity.

The selection of amino acid residues for substitution is determined, in part, by computer modeling. Computer hardware and software are described herein for producing three-dimensional images of immunoglobulin molecules. In general, molecular models are produced starting from solved structures for immunoglobulin chains or domains thereof. The chains to be modeled are compared for amino acid sequence similarity with chains or domains of solved three-dimensional structures, and the chains or domains showing the greatest sequence similarity is/are selected as starting points for construction of the molecular model. Chains or domains sharing at least 50% sequence identity are selected for modeling, and preferably those sharing at least 60%, 70%, 80%, 90% sequence identity or more are selected for modeling. The solved starting structures are modified to allow for differences between the actual amino acids in the immunoglobulin chains or domains being modeled, and those in the starting structure. The modified structures are then assembled into a composite immunoglobulin. Finally, the model is refined by energy minimization and by verifying that all atoms are within appropriate distances from one another and that bond lengths and angles are within chemically acceptable limits.

The selection of amino acid residues for substitution can also be determined, in part, by examination of the characteristics of the amino acids at particular

locations, or empirical observation of the effects of substitution or mutagenesis of particular amino acids. For example, when an amino acid differs between a murine variable region framework residue and a selected human variable region framework residue, the human framework amino acid should usually be substituted by the equivalent framework amino acid from the mouse antibody when it is reasonably expected that the amino acid:

(1) noncovalently binds antigen directly,

(2) is adjacent to a CDR region,

(3) otherwise interacts with a CDR region (*e.g.*, is within about 3-6 Å of a CDR region as determined by computer modeling), or

(4) participates in the VL-VH interface.

Residues which "noncovalently bind antigen directly" include amino acids in positions in framework regions which are have a good probability of directly interacting with amino acids on the antigen according to established chemical forces, for example, by hydrogen bonding, Van der Waals forces, hydrophobic interactions, and the like.

CDR and framework regions are as defined by Kabat *et al.* or Chothia *et al.*, *supra*. When framework residues, as defined by Kabat *et al.*, *supra*, constitute structural loop residues as defined by Chothia *et al.*, *supra*, the amino acids present in the mouse antibody may be selected for substitution into the humanized antibody. Residues which are "adjacent to a CDR region" include amino acid residues in positions immediately adjacent to one or more of the CDRs in the primary sequence of the humanized immunoglobulin chain, for example, in positions immediately adjacent to a CDR as defined by Kabat, or a CDR as defined by Chothia (See *e.g.*, Chothia and Lesk JMB 196:901 (1987)). These amino acids are particularly likely to interact with the amino acids in the CDRs and, if chosen from the acceptor, to distort the donor CDRs and reduce affinity. Moreover, the adjacent amino acids may interact directly with the antigen (Amit *et al.*, Science, 233:747 (1986), which is incorporated herein by reference) and selecting these amino acids from the donor may be desirable to keep all the antigen contacts that provide affinity in the original antibody.

Residues that "otherwise interact with a CDR region" include those that are determined by secondary structural analysis to be in a spatial orientation sufficient to

effect a CDR region. In one embodiment, residues that "otherwise interact with a CDR region" are identified by analyzing a three-dimensional model of the donor immunoglobulin (*e.g.*, a computer-generated model). A three-dimensional model, typically of the original donor antibody, shows that certain amino acids outside of the CDRs are close to the CDRs and have a good probability of interacting with amino acids in the CDRs by hydrogen bonding, Van der Waals forces, hydrophobic interactions, etc. At those amino acid positions, the donor immunoglobulin amino acid rather than the acceptor immunoglobulin amino acid may be selected. Amino acids according to this criterion will generally have a side chain atom within about 3 angstrom units (Å) of some atom in the CDRs and must contain an atom that could interact with the CDR atoms according to established chemical forces, such as those listed above.

In the case of atoms that may form a hydrogen bond, the 3 Å is measured between their nuclei, but for atoms that do not form a bond, the 3 Å is measured between their Van der Waals surfaces. Hence, in the latter case, the nuclei must be within about 6 Å (3 Å plus the sum of the Van der Waals radii) for the atoms to be considered capable of interacting. In many cases the nuclei will be from 4 or 5 to 6 Å apart. In determining whether an amino acid can interact with the CDRs, it is preferred not to consider the last 8 amino acids of heavy chain CDR 2 as part of the CDRs, because from the viewpoint of structure, these 8 amino acids behave more as part of the framework.

Amino acids that are capable of interacting with amino acids in the CDRs, may be identified in yet another way. The solvent accessible surface area of each framework amino acid is calculated in two ways: (1) in the intact antibody, and (2) in a hypothetical molecule consisting of the antibody with its CDRs removed. A significant difference between these numbers of about 10 square angstroms or more shows that access of the framework amino acid to solvent is at least partly blocked by the CDRs, and therefore that the amino acid is making contact with the CDRs. Solvent accessible surface area of an amino acid may be calculated based on a three-dimensional model of an antibody, using algorithms known in the art (*e.g.*, Connolly, J. Appl. Cryst. 16:548 (1983) and Lee and Richards, J. Mol. Biol. 55:379 (1971), both of which are incorporated herein by reference). Framework amino acids may also occasionally interact with the CDRs indirectly, by affecting the conformation of another framework amino acid that in turn contacts the CDRs.

The amino acids at several positions in the framework are known to be capable of interacting with the CDRs in many antibodies (Chothia and Lesk, *supra*, Chothia *et al.*, *supra* and Tramontano *et al.*, J. Mol. Biol. 215:175 (1990), all of which are incorporated herein by reference). Notably, the amino acids at positions 2, 48, 64 and 71 of the light chain and 26-30, 71 and 94 of the heavy chain (numbering according to Kabat) are known to be capable of interacting with the CDRs in many antibodies. The amino acids at positions 35 in the light chain and 93 and 103 in the heavy chain are also likely to interact with the CDRs. At all these numbered positions, choice of the donor amino acid rather than the acceptor amino acid (when they differ) to be in the humanized immunoglobulin is preferred. On the other hand, certain residues capable of interacting with the CDR region, such as the first 5 amino acids of the light chain, may sometimes be chosen from the acceptor immunoglobulin without loss of affinity in the humanized immunoglobulin.

Residues which “participate in the VL-VH interface” or “packing residues” include those residues at the interface between VL and VH as defined, for example, by Novotny and Haber, Proc. Natl. Acad. Sci. USA, 82:4592-66 (1985) or Chothia *et al*, *supra*. Generally, unusual packing residues should be retained in the humanized antibody if they differ from those in the human frameworks.

In general, one or more of the amino acids fulfilling the above criteria is substituted. In some embodiments, all or most of the amino acids fulfilling the above criteria are substituted. Occasionally, there is some ambiguity about whether a particular amino acid meets the above criteria, and alternative variant immunoglobulins are produced, one of which has that particular substitution, the other of which does not. Alternative variant immunoglobulins so produced can be tested in any of the assays described herein for the desired activity, and the preferred immunoglobulin selected.

Usually the CDR regions in humanized antibodies are substantially identical, and more usually, identical to the corresponding CDR regions of the donor antibody. Although not usually desirable, it is sometimes possible to make one or more conservative amino acid substitutions of CDR residues without appreciably affecting the binding affinity of the resulting humanized immunoglobulin. By conservative substitutions is intended combinations such as gly, ala; val, ile, leu; asp, glu; asn, gln; ser, thr; lys, arg; and phe, tyr.

Additional candidates for substitution are acceptor human framework amino acids that are unusual or "rare" for a human immunoglobulin at that position. These amino acids can be substituted with amino acids from the equivalent position of the mouse donor antibody or from the equivalent positions of more typical human immunoglobulins. For example, substitution may be desirable when the amino acid in a human framework region of the acceptor immunoglobulin is rare for that position and the corresponding amino acid in the donor immunoglobulin is common for that position in human immunoglobulin sequences; or when the amino acid in the acceptor immunoglobulin is rare for that position and the corresponding amino acid in the donor immunoglobulin is also rare, relative to other human sequences. These criterion help ensure that an atypical amino acid in the human framework does not disrupt the antibody structure. Moreover, by replacing an unusual human acceptor amino acid with an amino acid from the donor antibody that happens to be typical for human antibodies, the humanized antibody may be made less immunogenic.

The term "rare", as used herein, indicates an amino acid occurring at that position in less than about 20% but usually less than about 10% of sequences in a representative sample of sequences, and the term "common", as used herein, indicates an amino acid occurring in more than about 25% but usually more than about 50% of sequences in a representative sample. For example, all human light and heavy chain variable region sequences are respectively grouped into "subgroups" of sequences that are especially homologous to each other and have the same amino acids at certain critical positions (Kabat *et al., supra*). When deciding whether an amino acid in a human acceptor sequence is "rare" or "common" among human sequences, it will often be preferable to consider only those human sequences in the same subgroup as the acceptor sequence.

Additional candidates for substitution are acceptor human framework amino acids that would be identified as part of a CDR region under the alternative definition proposed by Chothia *et al., supra*. Additional candidates for substitution are acceptor human framework amino acids that would be identified as part of a CDR region under the AbM and/or contact definitions. Notably, CDR1 in the variable heavy chain is defined as including residues 26-32.

Additional candidates for substitution are acceptor framework residues that correspond to a rare or unusual donor framework residue. Rare or unusual donor framework residues are those that are rare or unusual (as defined herein) for murine antibodies at that position. For murine antibodies, the subgroup can be determined according to Kabat and residue positions identified which differ from the consensus. These donor specific differences may point to somatic mutations in the murine sequence which enhance activity. Unusual residues that are predicted to affect binding are retained, whereas residues predicted to be unimportant for binding can be substituted.

Additional candidates for substitution are non-germline residues occurring in an acceptor framework region. For example, when an acceptor antibody chain (*i.e.*, a human antibody chain sharing significant sequence identity with the donor antibody chain) is aligned to a germline antibody chain (likewise sharing significant sequence identity with the donor chain), residues not matching between acceptor chain framework and the germline chain framework can be substituted with corresponding residues from the germline sequence.

Other than the specific amino acid substitutions discussed above, the framework regions of humanized immunoglobulins are usually substantially identical, and more usually, identical to the framework regions of the human antibodies from which they were derived. Of course, many of the amino acids in the framework region make little or no direct contribution to the specificity or affinity of an antibody. Thus, many individual conservative substitutions of framework residues can be tolerated without appreciable change of the specificity or affinity of the resulting humanized immunoglobulin. Thus, in one embodiment the variable framework region of the humanized immunoglobulin shares at least 85% sequence identity to a human variable framework region sequence or consensus of such sequences. In another embodiment, the variable framework region of the humanized immunoglobulin shares at least 90%, preferably 95%, more preferably 96%, 97%, 98% or 99% sequence identity to a human variable framework region sequence or consensus of such sequences. In general, however, such substitutions are undesirable.

The humanized antibodies preferably exhibit a specific binding affinity for antigen of at least 10^7, 10^8, 10^9 or 10^{10} M^{-1}. Usually the upper limit of binding affinity of the humanized antibodies for antigen is within a factor of three, four or five of

that of the donor immunoglobulin. Often the lower limit of binding affinity is also within a factor of three, four or five of that of donor immunoglobulin. Alternatively, the binding affinity can be compared to that of a humanized antibody having no substitutions (*e.g.*, an antibody having donor CDRs and acceptor FRs, but no FR substitutions). In such instances, the binding of the optimized antibody (with substitutions) is preferably at least two- to three-fold greater, or three- to four-fold greater, than that of the unsubstituted antibody. For making comparisons, activity of the various antibodies can be determined, for example, by BIACORE (*i.e.*, surface plasmon resonance using unlabelled reagents) or competitive binding assays.

C. Production of Humanized 3D6 Antibodies

A preferred embodiment of the present invention features a humanized antibody to the N-terminus of Aβ, in particular, for use in the therapeutic and/or diagnostic methodologies described herein. A particularly preferred starting material for production of humanized antibodies is 3D6. 3D6 is specific for the N-terminus of Aβ and has been shown to mediate phagocytosis (*e.g.*, induce phagocytosis) of amyloid plaque (see Examples I-V). The cloning and sequencing of cDNA encoding the 3D6 antibody heavy and light chain variable regions is described in Example VI.

Suitable human acceptor antibody sequences are identified by computer comparisons of the amino acid sequences of the mouse variable regions with the sequences of known human antibodies. The comparison is performed separately for heavy and light chains but the principles are similar for each. In particular, variable domains from human antibodies whose framework sequences exhibit a high degree of sequence identity with the murine VL and VH framework regions were identified by query of the Kabat Database using NCBI BLAST (publicly accessible through the National Institutes of Health NCBI internet server) with the respective murine framework sequences. In one embodiment, acceptor sequences sharing greater that 50% sequence identity with murine donor sequences are selected. Preferably, acceptor antibody sequences sharing 60%, 70%, 80%, 90% or more are selected.

A computer comparison of 3D6 revealed that the 3D6 light chain shows the greatest sequence identity to human light chains of subtype kappa II, and that the 3D6 heavy chain shows greatest sequence identity to human heavy chains of subtype III,

as defined by Kabat *et al.*, *supra*. Thus, light and heavy human framework regions are preferably derived from human antibodies of these subtypes, or from consensus sequences of such subtypes. The preferred light chain human variable regions showing greatest sequence identity to the corresponding region from 3D6 are from antibodies having Kabat ID Numbers 019230, 005131, 005058, 005057, 005059, U21040 and U41645, with 019230 being more preferred. The preferred heavy chain human variable regions showing greatest sequence identity to the corresponding region from 3D6 are from antibodies having Kabat ID Numbers 045919, 000459, 000553, 000386 and M23691, with 045919 being more preferred.

Residues are next selected for substitution, as follows. When an amino acid differs between a 3D6 variable framework region and an equivalent human variable framework region, the human framework amino acid should usually be substituted by the equivalent mouse amino acid if it is reasonably expected that the amino acid:

(1) noncovalently binds antigen directly,

(2) is adjacent to a CDR region, is part of a CDR region under the alternative definition proposed by Chothia *et al.*, *supra*, or otherwise interacts with a CDR region (*e.g.*, is within about 3A of a CDR region) (*e.g.*, amino acids at positions L2, H49 and H94 of 3D6), or

(3) participates in the VL-VH interface (*e.g.*, amino acids at positions L36, L46 and H93 of 3D6).

Computer modeling of the 3D6 antibody heavy and light chain variable regions, and humanization of the 3D6 antibody is described in Example VII. Briefly, a three-dimensional model was generated based on the closest solved murine antibody structures for the heavy and light chains. For this purpose, an antibody designated 1CR9 (Protein Data Bank (PDB) ID: 1CR9, Kanyo *et al., J. Mol. Biol.* 293:855 (1999)) was chosen as a template for modeling the 3D6 light chain, and an antibody designated 1OPG (PDB ID: 1OPG, Kodandapani *et al., J. Biol. Chem.* 270:2268 (1995)) was chosen as the template for modeling the heavy chain. The model was further refined by a series of energy minimization steps to relieve unfavorable atomic contacts and optimize electrostatic and van der Walls interactions. The solved structure of 1qkz (PDB ID: 1QKZ, Derrick *et al., J. Mol. Biol.* 293:81 (1999)) was chosen as a template

for modeling CDR3 of the heavy chain as 3D6 and 1OPG did not exhibit significant sequence homology in this region when aligned for comparison purposes.

Three-dimensional structural information for the antibodies described herein is publicly available, for example, from the Research Collaboratory for Structural Bioinformatics' Protein Data Bank (PDB). The PDB is freely accessible *via* the World Wide Web internet and is described by Berman *et al.* (2000) *Nucleic Acids Research*, 28:235. Computer modeling allows for the identification of CDR-interacting residues. The computer model of the structure of 3D6 can in turn serve as a starting point for predicting the three-dimensional structure of an antibody containing the 3D6 complementarity determining regions substituted in human framework structures. Additional models can be constructed representing the structure as further amino acid substitutions are introduced.

In general, substitution of one, most or all of the amino acids fulfilling the above criteria is desirable. Accordingly, the humanized antibodies of the present invention will usually contain a substitution of a human light chain framework residue with a corresponding 3D6 residue in at least 1, 2 or 3, and more usually 4, of the following positions: L1, L2, L36 and L46. The humanized antibodies also usually contain a substitution of a human heavy chain framework residue with a corresponding 3D6 residue in at least 1, 2, and sometimes 3, of the following positions: H49, H93 and H94. Humanized antibodies can also contain a substitution of a heavy chain framework residue with a corresponding germline residue in at least 1, 2, and sometimes 3, of the following positions: H74, H77 and H89.

Occasionally, however, there is some ambiguity about whether a particular amino acid meets the above criteria, and alternative variant immunoglobulins are produced, one of which has that particular substitution, the other of which does not. In instances where substitution with a murine residue would introduce a residue that is rare in human immunoglobulins at a particular position, it may be desirable to test the antibody for activity with or without the particular substitution. If activity (*e.g.*, binding affinity and/or binding specificity) is about the same with or without the substitution, the antibody without substitution may be preferred, as it would be expected to elicit less of a HAHA response, as described herein.

Other candidates for substitution are acceptor human framework amino acids that are unusual for a human immunoglobulin at that position. These amino acids can be substituted with amino acids from the equivalent position of more typical human immunoglobulins. Alternatively, amino acids from equivalent positions in the mouse 3D6 can be introduced into the human framework regions when such amino acids are typical of human immunoglobulin at the equivalent positions.

In additional embodiments, when the human light chain framework acceptor immunoglobulin is Kabat ID Number 019230, the light chain contains substitutions in at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12 or more usually 13, of the following positions: L7, L10, L12, L15, L17, L39, L45, L63, L78, L83, L85, L100 or L104. In additional embodiments when the human heavy chain framework acceptor immunoglobulin is Kabat ID Number 045919, the heavy chain contains substitutions in at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or more usually 15, of the following positions: H3, H5, H13, H16, H19, H40, H41, H42, H44, H72, H77, H82A, H83, H84, or H108. These positions are substituted with the amino acid from the equivalent position of a human immunoglobulin having a more typical amino acid residue. Examples of appropriate amino acids to substitute are shown in Figures 1 and 2.

Other candidates for substitution are non-germline residues occurring in a framework region. A computer comparison of 3D6 with known germline sequences revealed that heavy chains showing the greatest degree of sequence identity include germline variable region sequences VH3-48, VH3-23, VH3-7, VH3-21 and VH3-11, with VH3-23 being more preferred. Alignment of Kabat ID 045919 with VH3-23 reveals that residues H74, H77 and/or H89 may be selected for substitution with corresponding germline residues (*e.g.*, residues H74, H77 and/or H89 when comparing Kabat ID 045919 and VH3-23). Likewise, germline sequences having the greatest degree of identity to the 3D6 light chain include A1, A17, A18, A2 and A19, with A19 being most preferred. Residues not matching between a selected light chain acceptor framework and one of these germline sequences could be selected for substitution with the corresponding germline residue.

Table 1 summarizes the sequence analysis of the 3D6 VH and VL regions. Additional mouse and human structures that can be used for computer modeling of the 3D6 antibody and additional human antibodies are set forth as well as

germline sequences that can be used in selecting amino acid substitutions. Rare mouse residues are also set forth in Table 1. Rare mouse residues are identified by comparing the donor VL and/or VH sequences with the sequences of other members of the subgroup to which the donor VL and/or VH sequences belong (according to Kabat) and identifying the residue positions which differ from the consensus. These donor specific differences may point to somatic mutations which enhance activity. Unusual or rare residues close to the binding site may possibly contact the antigen, making it desirable to retain the mouse residue. However, if the unusual mouse residue is not important for binding, use of the corresponding acceptor residue is preferred as the mouse residue may create immunogenic neoepitopes in the humanized antibody. In the situation where an unusual residue in the donor sequence is actually a common residues in the corresponding acceptor sequence, the preferred residue is clearly the acceptor residue.

Table 1: Summary of 3D6 V-region sequence

Chain	Heavy	Light
Mouse subgroup (Kabat seq ID#)	IIID (002688)	II (005840-005844, 005851-005853, 005857, 005863)
Mouse homologs (Kabat/Genbank)	002727/163.1'CL 002711/H35-C6'CL 002733/8-1-12-5-3-1(A2-1)'CL 002715/ASWA2'CL 020669/#14'CL	005840/1210.7 005843/42.4b.12.2'CL 005842/BXW-14'CL 005841/42.7B3.2'CL 005851/36-60CRI-
Rare amino acids (% frequency of occurrence in class)	N40 (0.233%) D42 (0.699%)	Y1(.035%) I15 (3.3%) D27 (0.867%)-CDR1 I78 (0.677%) L85 (0.625%) W89 (0.815%)-CDR3 K106A (0.295%)
Human Subgroup	III (000488-000491, 000503, 000624)	II (005046)
Chothia canonical CDR groupings [pdb example]	H1: class 1 [2fbj] H2: class 3 [1igc]	L1: class 4 [1rmf] L2: class1 [1lmk] L3: class 1 [1tet]
Closest solved mouse structures	PDB ID: 1OPG Kodandapani *et al., supra*; (72% 2Å)	PDB ID: 1CR9; Kanyo *et al., supra*; (94%, 2Å) PDB ID: 1NLD; Davies *et al., Acta Crystallogr. D. Biol. Crystallog.* 53:186

		(1997); (98%, 2.8Å)
Closest solved human structures	1VH (68%, nmr) 443560 (65%, IgG, λ myeloma, 1.8Å) KOL/2FB4H (60%, myeloma, 3Å)	1LVE (57%, LEN) 1B6DA (54%, B-J dimer, 2.8Å); 1VGEL (54%, autoAb)
Germline query (Hu) results (top 4)	VH3-48 (4512283/BAA75032.1) VH3-23 (4512287/BAA75046.1) VH3-7 (4512300/BAA75056.1) VH3-21 (4512287/BAA75047.1) VH3-11 (4152300/BAA75053.1)	A1(x63402) A17 (x63403) A18 (X63396) A2 (m31952) A19 (x63397)

*heavy chain and light chain from the same antibody (O-81, Hirabayashi *et al.* NAR 20:2601).

Kabat ID sequences referenced herein are publicly available, for example, from the Northwestern University Biomedical Engineering Department's Kabat Database of Sequences of Proteins of Immunological Interest. Three-dimensional structural information for antibodies described herein is publicly available, for example, from the Research Collaboratory for Structural Bioinformatics' Protein Data Bank (PDB). The PDB is freely accessible *via* the World Wide Web internet and is described by Berman *et al.* (2000) *Nucleic Acids Research*, p235-242. Germline gene sequences referenced herein are publicly available, for example, from the National Center for Biotechnology Information (NCBI) database of sequences in collections of Igh, Ig kappa and Ig lambda germline V genes (as a division of the National Library of Medicine (NLM) at the National Institutes of Health (NIH)). Homology searching of the NCBI "Ig Germline Genes" database is provided by IgG BLAST™.

In a preferred embodiment, a humanized antibody of the present invention contains (i) a light chain comprising a variable domain comprising murine 3D6 VL CDRs and a human acceptor framework, the framework having at least one, preferably two, three or four residues selected from the group consisting of L1, L2, L36, and L46 substituted with the corresponding 3D6 residue and (ii) a heavy chain comprising 3D6 VH CDRs and a human acceptor framework, the framework having at least one, preferably two or three residues selected from the group consisting of H49, H93 and H94 substituted with the corresponding 3D6 residue, and, optionally, at least one, preferably two or three residues selected from the group consisting of H74, H77 and H89 is substituted with a corresponding human germline residue..

In a more preferred embodiment, a humanized antibody of the present invention contains (i) a light chain comprising a variable domain comprising murine 3D6 VL CDRs and a human acceptor framework, the framework having residue 1 substituted with a tyr (Y), residue 2 substituted with a val (V), residue 36 substituted with a leu (L) and/or residue 46 substituted with an arg (R), and (ii) a heavy chain comprising 3D6 VH CDRs and a human acceptor framework, the framework having residue 49 substituted with an ala (A), residue 93 substituted with a val (V) and/or residue 94 substituted with an arg (R), and, optionally, having residue 74 substituted with a ser (S), residue 77 substituted with a thr (T) and/or residue 89 substituted with a val (V).

In a particularly preferred embodiment, a humanized antibody of the present invention has structural features, as described herein, and further has at least one (preferably two, three, four or all) of the following activities: (1) binds aggregated Aβ1-42 (*e.g.*, as determined by ELISA); (2) binds Aβ in plaques (*e.g.*, staining of AD and/or PDAPP plaques); (3) binds Aβ with two- to three- fold higher binding affinity as compared to chimeric 3D6 (*e.g.*, 3D6 having murine variable region sequences and human constant region sequences); (4) mediates phagocytosis of Aβ (*e.g.*, in an *ex vivo* phagocytosis assay, as described herein); and (5) crosses the blood-brain barrier (*e.g.*, demonstrates short-term brain localization, for example, in a PDAPP animal model, as described herein).

In another embodiment, a humanized antibody of the present invention has structural features, as described herein, binds Aβ in a manner or with an affinity sufficient to elicit at least one of the following *in vivo* effects: (1) reduce Aβ plaque burden; (2) prevent plaque formation; (3) reduce levels of soluble Aβ; (4) reduce the neuritic pathology associated with an amyloidogenic disorder; (5) lessens or ameliorate at least one physiological symptom associated with an amyloidogenic disorder; and/or (6) improves cognitive function.

In another embodiment, a humanized antibody of the present invention has structural features, as described herein, and specifically binds to an epitope comprising residues 1-5 or 3-7 of Aβ.

The activities described above can be determined utilizing any one of a variety of assays described herein or in the art (*e.g.*, binding assays, phagocytosis assays,

etc.). Activities can be assayed either *in vivo* (*e.g.*, using labeled assay components and/or imaging techniques) or *in vitro* (*e.g.*, using samples or specimens derived from a subject). Activities can be assayed either directly or indirectly. In certain preferred embodiments, neurological endpoints (*e.g.*, amyloid burden, neuritic burden, etc) are assayed. Such endpoints can be assayed in living subjects (*e.g.*, in animal models of Alzheimer's disease or in human subjects, for example, undergoing immunotherapy) using non-invasive detection methodologies. Alternatively, such endpoints can be assayed in subjects post mortem. Assaying such endpoints in animal models and/or in human subjects post mortem is useful in assessing the effectiveness of various agents (*e.g.*, humanized antibodies) to be utilized in similar immunotherapeutic applications. In other preferred embodiments, behavioral or neurological parameters can be assessed as indicators of the above neuropathological activities or endpoints.

3. Human Antibodies

Human antibodies against Aβ are provided by a variety of techniques, described below. Some human antibodies are selected by competitive binding experiments, or otherwise, to have the same epitope specificity as a particular mouse antibody, such as one of the mouse monoclonals described herein. Human antibodies can also be screened for a particular epitope specificity by using only a fragment of Aβ as the immunogen, and/or by screening antibodies against a collection of deletion mutants of Aβ. Human antibodies preferably have human IgG1 isotype specificity.

a. Trioma Methodology

The basic approach and an exemplary cell fusion partner, SPAZ-4, for use in this approach have been described by Oestberg *et al.*, Hybridoma 2:361 (1983); Oestberg, US Patent No. 4,634,664; and Engleman *et al.*, US Patent 4,634,666 (each of which is incorporated by reference in its entirety for all purposes). The antibody-producing cell lines obtained by this method are called triomas, because they are descended from three cells; two human and one mouse. Initially, a mouse myeloma line is fused with a human B-lymphocyte to obtain a non-antibody-producing xenogeneic hybrid cell, such as the SPAZ-4 cell line described by Oestberg, *supra*. The xenogeneic cell is then fused with an immunized human B-lymphocyte to obtain an antibody-

producing trioma cell line. Triomas have been found to produce antibody more stably than ordinary hybridomas made from human cells.

The immunized B-lymphocytes are obtained from the blood, spleen, lymph nodes or bone marrow of a human donor. If antibodies against a specific antigen or epitope are desired, it is preferable to use that antigen or epitope thereof for immunization. Immunization can be either *in vivo* or *in vitro*. For *in vivo* immunization, B cells are typically isolated from a human immunized with Aβ, a fragment thereof, larger polypeptide containing Aβ or fragment, or an anti-idiotypic antibody to an antibody to Aβ. In some methods, B cells are isolated from the same patient who is ultimately to be administered antibody therapy. For *in vitro* immunization, B-lymphocytes are typically exposed to antigen for a period of 7-14 days in a media such as RPMI-1640 (see Engleman, *supra*) supplemented with 10% human plasma.

The immunized B-lymphocytes are fused to a xenogeneic hybrid cell such as SPAZ-4 by well-known methods. For example, the cells are treated with 40-50% polyethylene glycol of MW 1000-4000, at about 37 degrees C, for about 5-10 min. Cells are separated from the fusion mixture and propagated in media selective for the desired hybrids (*e.g.*, HAT or AH). Clones secreting antibodies having the required binding specificity are identified by assaying the trioma culture medium for the ability to bind to Aβ or a fragment thereof. Triomas producing human antibodies having the desired specificity are subcloned by the limiting dilution technique and grown *in vitro* in culture medium. The trioma cell lines obtained are then tested for the ability to bind Aβ or a fragment thereof.

Although triomas are genetically stable they do not produce antibodies at very high levels. Expression levels can be increased by cloning antibody genes from the trioma into one or more expression vectors, and transforming the vector into standard mammalian, bacterial or yeast cell lines.

b. Transgenic Non-Human Mammals

Human antibodies against Aβ can also be produced from non-human transgenic mammals having transgenes encoding at least a segment of the human immunoglobulin locus. Usually, the endogenous immunoglobulin locus of such transgenic mammals is functionally inactivated. Preferably, the segment of the human immunoglobulin locus includes unrearranged sequences of heavy and light chain

components. Both inactivation of endogenous immunoglobulin genes and introduction of exogenous immunoglobulin genes can be achieved by targeted homologous recombination, or by introduction of YAC chromosomes. The transgenic mammals resulting from this process are capable of functionally rearranging the immunoglobulin component sequences, and expressing a repertoire of antibodies of various isotypes encoded by human immunoglobulin genes, without expressing endogenous immunoglobulin genes. The production and properties of mammals having these properties are described in detail by, *e.g.*, Lonberg *et al.*, WO93/12227 (1993); US 5,877,397, US 5,874,299, US 5,814,318, US 5,789,650, US 5,770,429, US 5,661,016, US 5,633,425, US 5,625,126, US 5,569,825, US 5,545,806, *Nature* 148:1547 (1994), *Nature Biotechnology* 14:826 (1996), Kucherlapati, WO 91/10741 (1991) (each of which is incorporated by reference in its entirety for all purposes). Transgenic mice are particularly suitable. Anti-Aβ antibodies are obtained by immunizing a transgenic nonhuman mammal, such as described by Lonberg or Kucherlapati, *supra,* with Aβ or a fragment thereof. Monoclonal antibodies are prepared by, *e.g.*, fusing B-cells from such mammals to suitable myeloma cell lines using conventional Kohler-Milstein technology. Human polyclonal antibodies can also be provided in the form of serum from humans immunized with an immunogenic agent. Optionally, such polyclonal antibodies can be concentrated by affinity purification using Aβ or other amyloid peptide as an affinity reagent.

c. Phage Display Methods

A further approach for obtaining human anti-Aβ antibodies is to screen a DNA library from human B cells according to the general protocol outlined by Huse *et al.*, *Science* 246:1275-1281 (1989). As described for trioma methodology, such B cells can be obtained from a human immunized with Aβ, fragments, longer polypeptides containing Aβ or fragments or anti-idiotypic antibodies. Optionally, such B cells are obtained from a patient who is ultimately to receive antibody treatment. Antibodies binding to Aβ or a fragment thereof are selected. Sequences encoding such antibodies (or a binding fragments) are then cloned and amplified. The protocol described by Huse is rendered more efficient in combination with phage-display technology. See, *e.g.*, Dower *et al.*, WO 91/17271, McCafferty *et al.*, WO 92/01047, Herzig *et al.*, US

5,877,218, Winter *et al.*, US 5,871,907, Winter *et al.*, US 5,858,657, Holliger *et al.*, US 5,837,242, Johnson *et al.*, US 5,733,743 and Hoogenboom *et al.*, US 5,565,332 (each of which is incorporated by reference in its entirety for all purposes). In these methods, libraries of phage are produced in which members display different antibodies on their outer surfaces. Antibodies are usually displayed as Fv or Fab fragments. Phage displaying antibodies with a desired specificity are selected by affinity enrichment to an Aβ peptide or fragment thereof.

In a variation of the phage-display method, human antibodies having the binding specificity of a selected murine antibody can be produced. See Winter, WO 92/20791. In this method, either the heavy or light chain variable region of the selected murine antibody is used as a starting material. If, for example, a light chain variable region is selected as the starting material, a phage library is constructed in which members display the same light chain variable region (*i.e.*, the murine starting material) and a different heavy chain variable region. The heavy chain variable regions are obtained from a library of rearranged human heavy chain variable regions. A phage showing strong specific binding for Aβ (*e.g.*, at least 10^8 and preferably at least 10^9 M^{-1}) is selected. The human heavy chain variable region from this phage then serves as a starting material for constructing a further phage library. In this library, each phage displays the same heavy chain variable region (*i.e.*, the region identified from the first display library) and a different light chain variable region. The light chain variable regions are obtained from a library of rearranged human variable light chain regions. Again, phage showing strong specific binding for Aβ are selected. These phage display the variable regions of completely human anti-Aβ antibodies. These antibodies usually have the same or similar epitope specificity as the murine starting material.

4. Production of Variable Regions

Having conceptually selected the CDR and framework components of humanized immunoglobulins, a variety of methods are available for producing such immunoglobulins. Because of the degeneracy of the code, a variety of nucleic acid sequences will encode each immunoglobulin amino acid sequence. The desired nucleic acid sequences can be produced by *de novo* solid-phase DNA synthesis or by PCR mutagenesis of an earlier prepared variant of the desired polynucleotide.

Oligonucleotide-mediated mutagenesis is a preferred method for preparing substitution, deletion and insertion variants of target polypeptide DNA. See Adelman *et al.*, DNA 2:183 (1983). Briefly, the target polypeptide DNA is altered by hybridizing an oligonucleotide encoding the desired mutation to a single-stranded DNA template. After hybridization, a DNA polymerase is used to synthesize an entire second complementary strand of the template that incorporates the oligonucleotide primer, and encodes the selected alteration in the target polypeptide DNA.

5. Selection of Constant Regions

The variable segments of antibodies produced as described *supra* (*e.g.*, the heavy and light chain variable regions of chimeric, humanized, or human antibodies) are typically linked to at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin. Human constant region DNA sequences can be isolated in accordance with well known procedures from a variety of human cells, but preferably immortalized B cells (see Kabat *et al.*, *supra*, and Liu *et al.*, W087/02671) (each of which is incorporated by reference in its entirety for all purposes). Ordinarily, the antibody will contain both light chain and heavy chain constant regions. The heavy chain constant region usually includes CH1, hinge, CH2, CH3, and CH4 regions. The antibodies described herein include antibodies having all types of constant regions, including IgM, IgG, IgD, IgA and IgE, and any isotype, including IgGl, IgG2, IgG3 and IgG4. The choice of constant region depends, in part, whether antibody-dependent complement and/or cellular mediated toxicity is desired. For example, isotopes IgG1 and IgG3 have complement activity and isotypes IgG2 and IgG4 do not. When it is desired that the antibody (*e.g.*, humanized antibody) exhibit cytotoxic activity, the constant domain is usually a complement fixing constant domain and the class is typically IgG1. When such cytotoxic activity is not desirable, the constant domain may be of the IgG2 class. Choice of isotype can also affect passage of antibody into the brain. Human isotype IgG1 is preferred. Light chain constant regions can be lambda or kappa. The humanized antibody may comprise sequences from more than one class or isotype. Antibodies can be expressed as tetramers containing two light and two heavy chains, as separate heavy chains, light chains, as Fab, Fab' F(ab')2, and Fv, or as single

chain antibodies in which heavy and light chain variable domains are linked through a spacer.

6. Expression of Recombinant Antibodies

Chimeric, humanized and human antibodies are typically produced by recombinant expression. Nucleic acids encoding light and heavy chain variable regions, optionally linked to constant regions, are inserted into expression vectors. The light and heavy chains can be cloned in the same or different expression vectors. The DNA segments encoding immunoglobulin chains are operably linked to control sequences in the expression vector(s) that ensure the expression of immunoglobulin polypeptides. Expression control sequences include, but are not limited to, promoters (*e.g.*, naturally-associated or heterologous promoters), signal sequences, enhancer elements, and transcription termination sequences. Preferably, the expression control sequences are eukaryotic promoter systems in vectors capable of transforming or transfecting eukaryotic host cells. Once the vector has been incorporated into the appropriate host, the host is maintained under conditions suitable for high level expression of the nucleotide sequences, and the collection and purification of the crossreacting antibodies.

These expression vectors are typically replicable in the host organisms either as episomes or as an integral part of the host chromosomal DNA. Commonly, expression vectors contain selection markers (*e.g.*, ampicillin-resistance, hygromycin-resistance, tetracycline resistance or neomycin resistance) to permit detection of those cells transformed with the desired DNA sequences (see, *e.g.*, Itakura *et al.*, US Patent 4,704,362).

E. coli is one prokaryotic host particularly useful for cloning the polynucleotides (*e.g.*, DNA sequences) of the present invention. Other microbial hosts suitable for use include bacilli, such as *Bacillus subtilus*, and other enterobacteriaceae, such as *Salmonella*, *Serratia*, and various *Pseudomonas* species. In these prokaryotic hosts, one can also make expression vectors, which will typically contain expression control sequences compatible with the host cell (*e.g.*, an origin of replication). In addition, any number of a variety of well-known promoters will be present, such as the lactose promoter system, a tryptophan (trp) promoter system, a beta-lactamase promoter system, or a promoter system from phage lambda. The promoters will typically control

expression, optionally with an operator sequence, and have ribosome binding site sequences and the like, for initiating and completing transcription and translation.

Other microbes, such as yeast, are also useful for expression. *Saccharomyces* is a preferred yeast host, with suitable vectors having expression control sequences (*e.g.*, promoters), an origin of replication, termination sequences and the like as desired. Typical promoters include 3-phosphoglycerate kinase and other glycolytic enzymes. Inducible yeast promoters include, among others, promoters from alcohol dehydrogenase, isocytochrome C, and enzymes responsible for maltose and galactose utilization.

In addition to microorganisms, mammalian tissue cell culture may also be used to express and produce the polypeptides of the present invention (*e.g.*, polynucleotides encoding immunoglobulins or fragments thereof). See Winnacker, From Genes to Clones, VCH Publishers, N.Y., N.Y. (1987). Eukaryotic cells are actually preferred, because a number of suitable host cell lines capable of secreting heterologous proteins (*e.g.*, intact immunoglobulins) have been developed in the art, and include CHO cell lines, various Cos cell lines, HeLa cells, preferably, myeloma cell lines, or transformed B-cells or hybridomas. Preferably, the cells are nonhuman. Expression vectors for these cells can include expression control sequences, such as an origin of replication, a promoter, and an enhancer (Queen *et al.*, *Immunol. Rev.* 89:49 (1986)), and necessary processing information sites, such as ribosome binding sites, RNA splice sites, polyadenylation sites, and transcriptional terminator sequences. Preferred expression control sequences are promoters derived from immunoglobulin genes, SV40, adenovirus, bovine papilloma virus, cytomegalovirus and the like. See Co *et al.*, *J. Immunol.* 148:1149 (1992).

Alternatively, antibody-coding sequences can be incorporated in transgenes for introduction into the genome of a transgenic animal and subsequent expression in the milk of the transgenic animal (see, *e.g.*, Deboer *et al.*, US 5,741,957, Rosen, US 5,304,489, and Meade *et al.*, US 5,849,992). Suitable transgenes include coding sequences for light and/or heavy chains in operable linkage with a promoter and enhancer from a mammary gland specific gene, such as casein or beta lactoglobulin.

The vectors containing the polynucleotide sequences of interest (*e.g.*, the heavy and light chain encoding sequences and expression control sequences) can be

transferred into the host cell by well-known methods, which vary depending on the type of cellular host. For example, calcium chloride transfection is commonly utilized for prokaryotic cells, whereas calcium phosphate treatment, electroporation, lipofection, biolistics or viral-based transfection may be used for other cellular hosts. (See generally Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual* (Cold Spring Harbor Press, 2nd ed., 1989) (incorporated by reference in its entirety for all purposes). Other methods used to transform mammalian cells include the use of polybrene, protoplast fusion, liposomes, electroporation, and microinjection (see generally, Sambrook *et al.*, *supra*). For production of transgenic animals, transgenes can be microinjected into fertilized oocytes, or can be incorporated into the genome of embryonic stem cells, and the nuclei of such cells transferred into enucleated oocytes.

When heavy and light chains are cloned on separate expression vectors, the vectors are co-transfected to obtain expression and assembly of intact immunoglobulins. Once expressed, the whole antibodies, their dimers, individual light and heavy chains, or other immunoglobulin forms of the present invention can be purified according to standard procedures of the art, including ammonium sulfate precipitation, affinity columns, column chromatography, HPLC purification, gel electrophoresis and the like (see generally Scopes, Protein Purification (Springer-Verlag, N.Y., (1982)). Substantially pure immunoglobulins of at least about 90 to 95% homogeneity are preferred, and 98 to 99% or more homogeneity most preferred, for pharmaceutical uses.

7. Antibody Fragments

Also contemplated within the scope of the instant invention are antibody fragments. In one embodiment, fragments of non-human, chimeric and/or human antibodies are provided. In another embodiment, fragments of humanized antibodies are provided. Typically, these fragments exhibit specific binding to antigen with an affinity of at least 10^7, and more typically 10^8 or 10^9 M^{-1}. Humanized antibody fragments include separate heavy chains, light chains Fab, Fab' F(ab')2, Fabc, and Fv. Fragments are produced by recombinant DNA techniques, or by enzymatic or chemical separation of intact immunoglobulins.

8. Testing Antibodies for Therapeutic Efficacy in Animal Models

Groups of 7-9 month old PDAPP mice each are injected with 0.5 mg in PBS of polyclonal anti-Aβ or specific anti-Aβ monoclonal antibodies. All antibody preparations are purified to have low endotoxin levels. Monoclonals can be prepared against a fragment by injecting the fragment or longer form of Aβ into a mouse, preparing hybridomas and screening the hybridomas for an antibody that specifically binds to a desired fragment of Aβ without binding to other nonoverlapping fragments of Aβ.

Mice are injected intraperitoneally as needed over a 4 month period to maintain a circulating antibody concentration measured by ELISA titer of greater than 1/1000 defined by ELISA to Aβ42 or other immunogen. Titers are monitored and mice are euthanized at the end of 6 months of injections. Histochemistry, Aβ levels and toxicology are performed post mortem. Ten mice are used per group.

9. Screening Antibodies for Clearing Activity

The invention also provides methods of screening an antibody for activity in clearing an amyloid deposit or any other antigen, or associated biological entity, for which clearing activity is desired. To screen for activity against an amyloid deposit, a tissue sample from a brain of a patient with Alzheimer's disease or an animal model having characteristic Alzheimer's pathology is contacted with phagocytic cells bearing an Fc receptor, such as microglial cells, and the antibody under test in a medium *in vitro*. The phagocytic cells can be a primary culture or a cell line, such as BV-2, C8-B4, or THP-1. In some methods, the components are combined on a microscope slide to facilitate microscopic monitoring. In some methods, multiple reactions are performed in parallel in the wells of a microtiter dish. In such a format, a separate miniature microscope slide can be mounted in the separate wells, or a nonmicroscopic detection format, such as ELISA detection of Aβ can be used. Preferably, a series of measurements is made of the amount of amyloid deposit in the *in vitro* reaction mixture, starting from a baseline value before the reaction has proceeded, and one or more test values during the reaction. The antigen can be detected by staining, for example, with a fluorescently labeled antibody to Aβ or other component of amyloid plaques. The antibody used for staining may or may not be the same as the antibody being tested for

clearing activity. A reduction relative to baseline during the reaction of the amyloid deposits indicates that the antibody under test has clearing activity. Such antibodies are likely to be useful in preventing or treating Alzheimer's and other amyloidogenic diseases.

Analogous methods can be used to screen antibodies for activity in clearing other types of biological entities. The assay can be used to detect clearing activity against virtually any kind of biological entity. Typically, the biological entity has some role in human or animal disease. The biological entity can be provided as a tissue sample or in isolated form. If provided as a tissue sample, the tissue sample is preferably unfixed to allow ready access to components of the tissue sample and to avoid perturbing the conformation of the components incidental to fixing. Examples of tissue samples that can be tested in this assay include cancerous tissue, precancerous tissue, tissue containing benign growths such as warts or moles, tissue infected with pathogenic microorganisms, tissue infiltrated with inflammatory cells, tissue bearing pathological matrices between cells (*e.g.*, fibrinous pericarditis), tissue bearing aberrant antigens, and scar tissue. Examples of isolated biological entities that can be used include Aβ, viral antigens or viruses, proteoglycans, antigens of other pathogenic microorganisms, tumor antigens, and adhesion molecules. Such antigens can be obtained from natural sources, recombinant expression or chemical synthesis, among other means. The tissue sample or isolated biological entity is contacted with phagocytic cells bearing Fc receptors, such as monocytes or microglial cells, and an antibody to be tested in a medium. The antibody can be directed to the biological entity under test or to an antigen associated with the entity. In the latter situation, the object is to test whether the biological entity is vicariously phagocytosed with the antigen. Usually, although not necessarily, the antibody and biological entity (sometimes with an associated antigen), are contacted with each other before adding the phagocytic cells. The concentration of the biological entity and/or the associated antigen remaining in the medium, if present, is then monitored. A reduction in the amount or concentration of antigen or the associated biological entity in the medium indicates the antibody has a clearing response against the antigen and/or associated biological entity in conjunction with the phagocytic cells (see, *e.g.*, Example IV).

10. Chimeric / Humanized Antibodies Having Altered Effector Function

For the above-described antibodies of the invention comprising a constant region (Fc region), it may also be desirable to alter the effector function of the molecule. Generally, the effector function of an antibody resides in the constant or Fc region of the molecule which can mediate binding to various effector molecules, *e.g.*, complement proteins or Fc receptors. The binding of complement to the Fc region is important, for example, in the opsonization and lysis of cell pathogens and the activation of inflammatory responses. The binding of antibody to Fc receptors, for example, on the surface of effector cells can trigger a number of important and diverse biological responses including, for example, engulfment and destruction of antibody-coated pathogens or particles, clearance of immune complexes, lysis of antibody-coated target cells by killer cells (*i.e.*, antibody-dependent cell-mediated cytotoxicity, or ADCC), release of inflammatory mediators, placental transfer of antibodies, and control of immunoglobulin production.

Accordingly, depending on a particular therapeutic or diagnostic application, the above-mentioned immune functions, or only selected immune functions, may be desirable. By altering the Fc region of the antibody, various aspects of the effector function of the molecule, including enhancing or suppressing various reactions of the immune system, with beneficial effects in diagnosis and therapy, are achieved.

The antibodies of the invention can be produced which react only with certain types of Fc receptors, for example, the antibodies of the invention can be modified to bind to only certain Fc receptors, or if desired, lack Fc receptor binding entirely, by deletion or alteration of the Fc receptor binding site located in the Fc region of the antibody. Other desirable alterations of the Fc region of an antibody of the invention are cataloged below. Typically the Kabat numbering system is used to indicate which amino acid residue(s) of the Fc region (*e.g.*, of an IgG antibody) are altered (*e.g.*, by amino acid substitution) in order to achieve a desired change in effector function. The numbering system is also employed to compare antibodies across species such that a desired effector function observed in, for example, a mouse antibody, can then be systematically engineered into a human, humanized, or chimeric antibody of the invention.

For example, it has been observed that antibodies (*e.g.*, IgG antibodies) can be grouped into those found to exhibit tight, intermediate, or weak binding to an Fc receptor (*e.g.*, an Fc receptor on human monocytes (FcγRI)). By comparison of the amino-acid sequences in these different affinity groups, a monocyte-binding site in the hinge-link region (Leu234-Ser239) has been identified. Moreover, the human FcγRI receptor binds human IgG1 and mouse IgG2a as a monomer, but the binding of mouse IgG2b is 100-fold weaker. A comparison of the sequence of these proteins in the hinge-link region shows that the sequence 234 to 238, *i.e.*, Leu-Leu-Gly-Gly-Pro in the strong binders becomes Leu-Glu-Gly-Gly-Pro in mouse gamma 2b, *i.e.*, weak binders. Accordingly, a corresponding change in a human antibody hinge sequence can be made if reduced FcγI receptor binding is desired. It is understood that other alterations can be made to achieve the same or similar results. For example, the affinity of FcγRI binding can be altered by replacing the specified residue with a residue having an inappropriate functional group on its sidechain, or by introducing a charged functional group (*e.g.*, Glu or Asp) or for example an aromatic non-polar residue (*e.g.*, Phe, Tyr, or Trp).

These changes can be equally applied to the murine, human, and rat systems given the sequence homology between the different immunoglobulins. It has been shown that for human IgG3, which binds to the human FcγRI receptor, changing Leu 235 to Glu destroys the interaction of the mutant for the receptor. The binding site for this receptor can thus be switched on or switched off by making the appropriate mutation.

Mutations on adjacent or close sites in the hinge link region (*e.g.*, replacing residues 234, 236 or 237 by Ala) indicate that alterations in residues 234, 235, 236, and 237 at least affect affinity for the FcγRI receptor. Accordingly, the antibodies of the invention can also have an altered Fc region with altered binding affinity for FcγRI as compared with the unmodified antibody. Such an antibody conveniently has a modification at amino acid residue 234, 235, 236, or 237.

Affinity for other Fc receptors can be altered by a similar approach, for controlling the immune response in different ways.

As a further example, the lytic properties of IgG antibodies following binding of the Cl component of complement can be altered.

The first component of the complement system, Cl, comprises three proteins known as Clq, Clr and Cls which bind tightly together. It has been shown that Clq is responsible for binding of the three protein complex to an antibody.

Accordingly, the Clq binding activity of an antibody can be altered by providing an antibody with an altered CH 2 domain in which at least one of the amino acid residues 318, 320, and 322 of the heavy chain has been changed to a residue having a different side chain. The numbering of the residues in the heavy chain is that of the EU index (see Kabat *et al.*, supra). Other suitable alterations for altering, *e.g.*, reducing or abolishing specific Clq-binding to an antibody include changing any one of residues 318 (Glu), 320 (Lys) and 322 (Lys), to Ala.

Moreover, by making mutations at these residues, it has been shown that Clq binding is retained as long as residue 318 has a hydrogen-bonding side chain and residues 320 and 322 both have a positively charged side chain.

Clq binding activity can be abolished by replacing any one of the three specified residues with a residue having an inappropriate functionality on its side chain. It is not necessary to replace the ionic residues only with Ala to abolish Clq binding. It is also possible to use other alkyl-substituted non-ionic residues, such as Gly, Ile, Leu, or Val, or such aromatic non-polar residues as Phe, Tyr, Trp and Pro in place of any one of the three residues in order to abolish Clq binding. In addition, it is also be possible to use such polar non-ionic residues as Ser, Thr, Cys, and Met in place of residues 320 and 322, but not 318, in order to abolish Clq binding activity.

It is also noted that the side chains on ionic or non-ionic polar residues will be able to form hydrogen bonds in a similar manner to the bonds formed by the Glu residue. Therefore, replacement of the 318 (Glu) residue by a polar residue may modify but not abolish Clq binding activity.

It is also known that replacing residue 297 (Asn) with Ala results in removal of lytic activity while only slightly reducing (about three fold weaker) affinity for Clq. This alteration destroys the glycosylation site and the presence of carbohydrate that is required for complement activation. Any other substitution at this site will also destroy the glycosylation site.

The invention also provides an antibody having an altered effector function wherein the antibody has a modified hinge region. The modified hinge region

may comprise a complete hinge region derived from an antibody of different antibody class or subclass from that of the CH1 domain. For example, the constant domain (CH1) of a class IgG antibody can be attached to a hinge region of a class IgG4 antibody. Alternatively, the new hinge region may comprise part of a natural hinge or a repeating unit in which each unit in the repeat is derived from a natural hinge region. In one example, the natural hinge region is altered by converting one or more cysteine residues into a neutral residue, such as alanine, or by converting suitably placed residues into cysteine residues. Such alterations are carried out using art recognized protein chemistry and, preferably, genetic engineering techniques, as described herein.

In one embodiment of the invention, the number of cysteine residues in the hinge region of the antibody is reduced, for example, to one cysteine residue. This modification has the advantage of facilitating the assembly of the antibody, for example, bispecific antibody molecules and antibody molecules wherein the Fc portion has been replaced by an effector or reporter molecule, since it is only necessary to form a single disulfide bond. This modification also provides a specific target for attaching the hinge region either to another hinge region or to an effector or reporter molecule, either directly or indirectly, for example, by chemical means.

Conversely, the number of cysteine residues in the hinge region of the antibody is increased, for example, at least one more than the number of normally occurring cysteine residues. Increasing the number of cysteine residues can be used to stabilize the interactions between adjacent hinges. Another advantage of this modification is that it facilitates the use of cysteine thiol groups for attaching effector or reporter molecules to the altered antibody, for example, a radiolabel.

Accordingly, the invention provides for an exchange of hinge regions between antibody classes, in particular, IgG classes, and/or an increase or decrease in the number of cysteine residues in the hinge region in order to achieve an altered effector function (see for example U.S. Patent No. 5,677,425 which is expressly incorporated herein). A determination of altered antibody effector function is made using the assays described herein or other art recognized techniques.

Importantly, the resultant antibody can be subjected to one or more assays to evaluate any change in biological activity compared to the starting antibody. For example, the ability of the antibody with an altered Fc region to bind complement or

Fc receptors can be assessed using the assays disclosed herein as well as any art recognized assay.

Production of the antibodies of the invention is carried out by any suitable technique including techniques described herein as well as techniques known to those skilled in the art. For example an appropriate protein sequence, *e.g.* forming part of or all of a relevant constant domain, *e.g.*, Fc region, *i.e.*, CH2, and/or CH3 domain(s), of an antibody, and include appropriately altered residue(s) can be synthesized and then chemically joined into the appropriate place in an antibody molecule.

Preferably, genetic engineering techniques are used for producing an altered antibody. Preferred techniques include, for example, preparing suitable primers for use in polymerase chain reaction (PCR) such that a DNA sequence which encodes at least part of an IgG heavy chain, *e.g.*, an Fc or constant region (*e.g.*, CH2, and/or CH3) is altered, at one or more residues. The segment can then be operably linked to the remaining portion of the antibody, *e.g.*, the variable region of the antibody and required regulatory elements for expression in a cell.

The present invention also includes vectors used to transform the cell line, vectors used in producing the transforming vectors, cell lines transformed with the transforming vectors, cell lines transformed with preparative vectors, and methods for their production.

Preferably, the cell line which is transformed to produce the antibody with an altered Fc region (*i.e.*, of altered effector function) is an immortalized mammalian cell line (*e.g.*, CHO cell).

Although the cell line used to produce the antibody with an altered Fc region is preferably a mammalian cell line, any other suitable cell line, such as a bacterial cell line or a yeast cell line, may alternatively be used.

B. Nucleic Acid Encoding Immunologic and Therapeutic Agents

Immune responses against amyloid deposits can also be induced by administration of nucleic acids encoding antibodies and their component chains used for passive immunization. Such nucleic acids can be DNA or RNA. A nucleic acid segment encoding an immunogen is typically linked to regulatory elements, such as a

promoter and enhancer, that allow expression of the DNA segment in the intended target cells of a patient. For expression in blood cells, as is desirable for induction of an immune response, promoter and enhancer elements from light or heavy chain immunoglobulin genes or the CMV major intermediate early promoter and enhancer are suitable to direct expression. The linked regulatory elements and coding sequences are often cloned into a vector. For administration of double-chain antibodies, the two chains can be cloned in the same or separate vectors.

A number of viral vector systems are available including retroviral systems *(see, e.g.*, Lawrie and Tumin, *Cur. Opin. Genet. Develop.* 3:102-109 (1993)); adenoviral vectors (*see, e.g.*, Bett *et al.*, *J. Virol.* 67:5911 (1993)); adeno-associated virus vectors (see, *e.g.*, Zhou *et al.*, *J. Exp. Med.* 179:1867 (1994)), viral vectors from the pox family including vaccinia virus and the avian pox viruses, viral vectors from the alpha virus genus such as those derived from Sindbis and Semliki Forest Viruses *(see, e.g.*, Dubensky *et al.*, *J. Virol.* 70:508 (1996)), Venezuelan equine encephalitis virus (see Johnston *et al.*, US 5,643,576) and rhabdoviruses, such as vesicular stomatitis virus (see Rose, WO 96/34625)and papillomaviruses (Ohe *et al.*, *Human Gene Therapy* 6:325 (1995); Woo *et al.*, WO 94/12629 and Xiao & Brandsma, *Nucleic Acids. Res.* 24, 2630-2622 (1996)).

DNA encoding an immunogen, or a vector containing the same, can be packaged into liposomes. Suitable lipids and related analogs are described by Eppstein *et al.*, US 5,208,036, Felgner *et al.*, US 5,264,618, Rose, US 5,279,833, and Epand *et al.*, US 5,283,185. Vectors and DNA encoding an immunogen can also be adsorbed to or associated with particulate carriers, examples of which include polymethyl methacrylate polymers and polylactides and poly (lactide-co-glycolides), see, *e.g.*, McGee *et al.*, *J. Micro Encap.* (1996).

Gene therapy vectors or naked polypeptides (*e.g.*, DNA) can be delivered *in vivo* by administration to an individual patient, typically by systemic administration (*e.g.*, intravenous, intraperitoneal, nasal, gastric, intradermal, intramuscular, subdermal, or intracranial infusion) or topical application (*see e.g.*, Anderson *et al.*, US 5,399,346). The term "naked polynucleotide" refers to a polynucleotide not complexed with colloidal materials. Naked polynucleotides are sometimes cloned in a plasmid vector. Such vectors can further include facilitating agents such as bupivacine (Attardo *et al.*,

US 5,593,970). DNA can also be administered using a gene gun. See Xiao & Brandsma, *supra*. The DNA encoding an immunogen is precipitated onto the surface of microscopic metal beads. The microprojectiles are accelerated with a shock wave or expanding helium gas, and penetrate tissues to a depth of several cell layers. For example, The Accel™ Gene Delivery Device manufactured by Agacetus, Inc. Middleton WI is suitable. Alternatively, naked DNA can pass through skin into the blood stream simply by spotting the DNA onto skin with chemical or mechanical irritation (see Howell *et al.*, WO 95/05853).

In a further variation, vectors encoding immunogens can be delivered to cells *ex vivo*, such as cells explanted from an individual patient (*e.g.*, lymphocytes, bone marrow aspirates, tissue biopsy) or universal donor hematopoietic stem cells, followed by reimplantation of the cells into a patient, usually after selection for cells which have incorporated the vector.

II. Prophylactic and Therapeutic Methods

The present invention is directed *inter alia* to treatment of Alzheimer's and other amyloidogenic diseases by administration of therapeutic immunological reagents (*e.g.*, humanized immunoglobulins) to specific epitopes within Aβ to a patient under conditions that generate a beneficial therapeutic response in a patient (*e.g.*, induction of phagocytosis of Aβ, reduction of plaque burden, inhibition of plaque formation, reduction of neuritic dystrophy, improving cognitive function, and/or reversing, treating or preventing cognitive decline) in the patient, for example, for the prevention or treatment of an amyloidogenic disease. The invention is also directed to use of the disclosed immunological reagents (*e.g.*, humanized immunoglobulins) in the manufacture of a medicament for the treatment or prevention of an amyloidogenic disease.

The term "treatment" as used herein, is defined as the application or administration of a therapeutic agent to a patient, or application or administration of a therapeutic agent to an isolated tissue or cell line from a patient, who has a disease, a symptom of disease or a predisposition toward a disease, with the purpose to cure, heal, alleviate, relieve, alter, remedy, ameliorate, improve or affect the disease, the symptoms of disease or the predisposition toward disease.

In one aspect, the invention provides methods of preventing or treating a disease associated with amyloid deposits of Aβ in the brain of a patient. Such diseases include Alzheimer's disease, Down's syndrome and cognitive impairment. The latter can occur with or without other characteristics of an amyloidogenic disease. Some methods of the invention entail administering an effective dosage of an antibody that specifically binds to a component of an amyloid deposit to the patient. Such methods are particularly useful for preventing or treating Alzheimer's disease in human patients. Exemplary methods entail administering an effective dosage of an antibody that binds to Aβ. Preferred methods entail administering an effective dosage of an antibody that specifically binds to an epitope within residues 1-10 of Aβ, for example, antibodies that specifically bind to an epitope within residues 1-3 of Aβ, antibodies that specifically bind to an epitope within residues 1-4 of Aβ, antibodies that specifically bind to an epitope within residues 1-5 of Aβ, antibodies that specifically bind to an epitope within residues 1-6 of Aβ, antibodies that specifically bind to an epitope within residues 1-7 of Aβ, or antibodies that specifically bind to an epitope within residues 3-7 of Aβ. In yet another aspect, the invention features administering antibodies that bind to an epitope comprising a free N-terminal residue of Aβ. In yet another aspect, the invention features administering antibodies that bind to an epitope within residues of 1-10 of Aß wherein residue 1 and/or residue 7 of Aβ is aspartic acid. In yet another aspect, the invention features administering antibodies that specifically bind to Aβ peptide without binding to full-length amyloid precursor protein (APP). In yet another aspect, the isotype of the antibody is human IgG1.

In yet another aspect, the invention features administering antibodies that bind to an amyloid deposit in the patient and induce a clearing response against the amyloid deposit. For example, such a clearing response can be effected by Fc receptor mediated phagocytosis.

Therapeutic agents of the invention are typically substantially pure from undesired contaminant. This means that an agent is typically at least about 50% w/w (weight/weight) purity, as well as being substantially free from interfering proteins and contaminants. Sometimes the agents are at least about 80% w/w and, more preferably at least 90 or about 95% w/w purity. However, using conventional protein purification techniques, homogeneous peptides of at least 99% w/w can be obtained.

The methods can be used on both asymptomatic patients and those currently showing symptoms of disease. The antibodies used in such methods can be human, humanized, chimeric or nonhuman antibodies, or fragments thereof (*e.g.*, antigen binding fragments) and can be monoclonal or polyclonal, as described herein. In yet another aspect, the invention features administering antibodies prepared from a human immunized with Aβ peptide, which human can be the patient to be treated with antibody.

In another aspect, the invention features administering an antibody with a pharmaceutical carrier as a pharmaceutical composition. Alternatively, the antibody can be administered to a patient by administering a polynucleotide encoding at least one antibody chain. The polynucleotide is expressed to produce the antibody chain in the patient. Optionally, the polynucleotide encodes heavy and light chains of the antibody. The polynucleotide is expressed to produce the heavy and light chains in the patient. In exemplary embodiments, the patient is monitored for level of administered antibody in the blood of the patient.

The invention thus fulfills a longstanding need for therapeutic regimes for preventing or ameliorating the neuropathology and, in some patients, the cognitive impairment associated with Alzheimer's disease.

A. Patients Amenable to Treatment

Patients amenable to treatment include individuals at risk of disease but not showing symptoms, as well as patients presently showing symptoms. In the case of Alzheimer's disease, virtually anyone is at risk of suffering from Alzheimer's disease if he or she lives long enough. Therefore, the present methods can be administered prophylactically to the general population without the need for any assessment of the risk of the subject patient. The present methods are especially useful for individuals who have a known genetic risk of Alzheimer's disease. Such individuals include those having relatives who have experienced this disease, and those whose risk is determined by analysis of genetic or biochemical markers. Genetic markers of risk toward Alzheimer's disease include mutations in the APP gene, particularly mutations at position 717 and positions 670 and 671 referred to as the Hardy and Swedish mutations respectively (see Hardy, *supra*). Other markers of risk are mutations in the presenilin

genes, PS1 and PS2, and ApoE4, family history of AD, hypercholesterolemia or atherosclerosis. Individuals presently suffering from Alzheimer's disease can be recognized from characteristic dementia, as well as the presence of risk factors described above. In addition, a number of diagnostic tests are available for identifying individuals who have AD. These include measurement of CSF tau and Aβ42 levels. Elevated tau and decreased Aβ42 levels signify the presence of AD. Individuals suffering from Alzheimer's disease can also be diagnosed by ADRDA criteria as discussed in the Examples section.

In asymptomatic patients, treatment can begin at any age (*e.g.*, 10, 20, 30). Usually, however, it is not necessary to begin treatment until a patient reaches 40, 50, 60 or 70. Treatment typically entails multiple dosages over a period of time. Treatment can be monitored by assaying antibody levels over time. If the response falls, a booster dosage is indicated. In the case of potential Down's syndrome patients, treatment can begin antenatally by administering therapeutic agent to the mother or shortly after birth.

B. Treatment Regimes and Dosages

In prophylactic applications, pharmaceutical compositions or medicaments are administered to a patient susceptible to, or otherwise at risk of, Alzheimer's disease in an amount sufficient to eliminate or reduce the risk, lessen the severity, or delay the outset of the disease, including biochemical, histologic and/or behavioral symptoms of the disease, its complications and intermediate pathological phenotypes presenting during development of the disease. In therapeutic applications, compositions or medicants are administered to a patient suspected of, or already suffering from such a disease in an amount sufficient to cure, or at least partially arrest, the symptoms of the disease (biochemical, histologic and/or behavioral), including its complications and intermediate pathological phenotypes in development of the disease.

In some methods, administration of agent reduces or eliminates myocognitive impairment in patients that have not yet developed characteristic Alzheimer's pathology. An amount adequate to accomplish therapeutic or prophylactic treatment is defined as a therapeutically- or prophylactically-effective dose. In both prophylactic and therapeutic regimes, agents are usually administered in several dosages

until a sufficient immune response has been achieved. The term "immune response" or "immunological response" includes the development of a humoral (antibody mediated) and/or a cellular (mediated by antigen-specific T cells or their secretion products) response directed against an antigen in a recipient subject. Such a response can be an active response, *i.e.*, induced by administration of immunogen, or a passive response, *i.e.*, induced by administration of immunoglobulin or antibody or primed T-cells.

An "immunogenic agent" or "immunogen" is capable of inducing an immunological response against itself on administration to a mammal, optionally in conjunction with an adjuvant. Typically, the immune response is monitored and repeated dosages are given if the immune response starts to wane.

Effective doses of the compositions of the present invention, for the treatment of the above described conditions vary depending upon many different factors, including means of administration, target site, physiological state of the patient, whether the patient is human or an animal, other medications administered, and whether treatment is prophylactic or therapeutic. Usually, the patient is a human but non-human mammals including transgenic mammals can also be treated. Treatment dosages need to be titrated to optimize safety and efficacy.

For passive immunization with an antibody, the dosage ranges from about 0.0001 to 100 mg/kg, and more usually 0.01 to 5 mg/kg, of the host body weight. For example dosages can be 1 mg/kg body weight or 10 mg/kg body weight or within the range of 1-10 mg/kg, preferably at least 1 mg/kg. Subjects can be administered such doses daily, on alternative days, weekly or according to any other schedule determined by empirical analysis. An exemplary treatment entails administration in multiple dosages over a prolonged period, for example, of at least six months. Additional exemplary treatment regimes entail administration once per every two weeks or once a month or once every 3 to 6 months. Exemplary dosage schedules include 1-10 mg/kg or 15 mg/kg on consecutive days, 30 mg/kg on alternate days or 60 mg/kg weekly. In some methods, two or more monoclonal antibodies with different binding specificities are administered simultaneously, in which case the dosage of each antibody administered falls within the ranges indicated.

Antibody is usually administered on multiple occasions. Intervals between single dosages can be weekly, monthly or yearly. Intervals can also be

irregular as indicated by measuring blood levels of antibody to Aβ in the patient. In some methods, dosage is adjusted to achieve a plasma antibody concentration of 1-1000 μg/ml and in some methods 25-300 μg/ml. Alternatively, antibody can be administered as a sustained release formulation, in which case less frequent administration is required. Dosage and frequency vary depending on the half-life of the antibody in the patient. In general, human antibodies show the longest half-life, followed by humanized antibodies, chimeric antibodies, and nonhuman antibodies.

The dosage and frequency of administration can vary depending on whether the treatment is prophylactic or therapeutic. In prophylactic applications, compositions containing the present antibodies or a cocktail thereof are administered to a patient not already in the disease state to enhance the patient's resistance. Such an amount is defined to be a "prophylactic effective dose." In this use, the precise amounts again depend upon the patient's state of health and general immunity, but generally range from 0.1 to 25 mg per dose, especially 0.5 to 2.5 mg per dose. A relatively low dosage is administered at relatively infrequent intervals over a long period of time. Some patients continue to receive treatment for the rest of their lives.

In therapeutic applications, a relatively high dosage (*e.g.*, from about 1 to 200 mg of antibody per dose, with dosages of from 5 to 25 mg being more commonly used) at relatively short intervals is sometimes required until progression of the disease is reduced or terminated, and preferably until the patient shows partial or complete amelioration of symptoms of disease. Thereafter, the patent can be administered a prophylactic regime.

Doses for nucleic acids encoding antibodies range from about 10 ng to 1 g, 100 ng to 100 mg, 1 μg to 10 mg, or 30-300 μg DNA per patient. Doses for infectious viral vectors vary from 10-100, or more, virions per dose.

Therapeutic agents can be administered by parenteral, topical, intravenous, oral, subcutaneous, intraarterial, intracranial, intraperitoneal, intranasal or intramuscular means for prophylactic and/or therapeutic treatment. The most typical route of administration of an immunogenic agent is subcutaneous although other routes can be equally effective. The next most common route is intramuscular injection. This type of injection is most typically performed in the arm or leg muscles. In some methods, agents are injected directly into a particular tissue where deposits have

accumulated, for example intracranial injection. Intramuscular injection or intravenous infusion are preferred for administration of antibody. In some methods, particular therapeutic antibodies are injected directly into the cranium. In some methods, antibodies are administered as a sustained release composition or device, such as a Medipad™ device.

Agents of the invention can optionally be administered in combination with other agents that are at least partly effective in treatment of amyloidogenic disease. In the case of Alzheimer's and Down's syndrome, in which amyloid deposits occur in the brain, agents of the invention can also be administered in conjunction with other agents that increase passage of the agents of the invention across the blood-brain barrier.

C. Pharmaceutical Compositions

Agents of the invention are often administered as pharmaceutical compositions comprising an active therapeutic agent, *i.e.*, and a variety of other pharmaceutically acceptable components. See *Remington's Pharmaceutical Science* (15th ed., Mack Publishing Company, Easton, Pennsylvania (1980)). The preferred form depends on the intended mode of administration and therapeutic application. The compositions can also include, depending on the formulation desired, pharmaceutically-acceptable, non-toxic carriers or diluents, which are defined as vehicles commonly used to formulate pharmaceutical compositions for animal or human administration. The diluent is selected so as not to affect the biological activity of the combination. Examples of such diluents are distilled water, physiological phosphate-buffered saline, Ringer's solutions, dextrose solution, and Hank's solution. In addition, the pharmaceutical composition or formulation may also include other carriers, adjuvants, or nontoxic, nontherapeutic, nonimmunogenic stabilizers and the like.

Pharmaceutical compositions can also include large, slowly metabolized macromolecules such as proteins, polysaccharides such as chitosan, polylactic acids, polyglycolic acids and copolymers (such as latex functionalized sepharose(TM), agarose, cellulose, and the like), polymeric amino acids, amino acid copolymers, and lipid aggregates (such as oil droplets or liposomes). Additionally, these carriers can function as immunostimulating agents (*i.e.*, adjuvants).

For parenteral administration, agents of the invention can be administered as injectable dosages of a solution or suspension of the substance in a physiologically acceptable diluent with a pharmaceutical carrier that can be a sterile liquid such as water oils, saline, glycerol, or ethanol. Additionally, auxiliary substances, such as wetting or emulsifying agents, surfactants, pH buffering substances and the like can be present in compositions. Other components of pharmaceutical compositions are those of petroleum, animal, vegetable, or synthetic origin, for example, peanut oil, soybean oil, and mineral oil. In general, glycols such as propylene glycol or polyethylene glycol are preferred liquid carriers, particularly for injectable solutions. Antibodies can be administered in the form of a depot injection or implant preparation, which can be formulated in such a manner as to permit a sustained release of the active ingredient. An exemplary composition comprises monoclonal antibody at 5 mg/mL, formulated in aqueous buffer consisting of 50 mM L-histidine, 150 mM NaCl, adjusted to pH 6.0 with HCl.

Typically, compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection can also be prepared. The preparation also can be emulsified or encapsulated in liposomes or micro particles such as polylactide, polyglycolide, or copolymer for enhanced adjuvant effect, as discussed above (see Langer, *Science* 249: 1527 (1990) and Hanes, *Advanced Drug Delivery Reviews* 28:97 (1997)). The agents of this invention can be administered in the form of a depot injection or implant preparation, which can be formulated in such a manner as to permit a sustained or pulsatile release of the active ingredient.

Additional formulations suitable for other modes of administration include oral, intranasal, and pulmonary formulations, suppositories, and transdermal applications. For suppositories, binders and carriers include, for example, polyalkylene glycols or triglycerides; such suppositories can be formed from mixtures containing the active ingredient in the range of 0.5% to 10%, preferably 1%-2%. Oral formulations include excipients, such as pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharine, cellulose, and magnesium carbonate. These compositions take the form of solutions, suspensions, tablets, pills, capsules, sustained

release formulations or powders and contain 10%-95% of active ingredient, preferably 25%-70%.

Topical application can result in transdermal or intradermal delivery. Topical administration can be facilitated by co-administration of the agent with cholera toxin or detoxified derivatives or subunits thereof or other similar bacterial toxins (See Glenn *et al.*, *Nature* 391, 851 (1998)). Co-administration can be achieved by using the components as a mixture or as linked molecules obtained by chemical crosslinking or expression as a fusion protein.

Alternatively, transdermal delivery can be achieved using a skin path or using transferosomes (Paul *et al.*, *Eur. J. Immunol.* 25:3521 (1995); Cevc *et al.*, *Biochem. Biophys. Acta* 1368:201-15 (1998)).

III. Monitoring the Course of Treatment

The invention provides methods of monitoring treatment in a patient suffering from or susceptible to Alzheimer's, *i.e.*, for monitoring a course of treatment being administered to a patient. The methods can be used to monitor both therapeutic treatment on symptomatic patients and prophylactic treatment on asymptomatic patients. In particular, the methods are useful for monitoring passive immunization (*e.g.*, measuring level of administered antibody).

Some methods entail determining a baseline value, for example, of an antibody level or profile in a patient, before administering a dosage of agent, and comparing this with a value for the profile or level after treatment. A significant increase (*i.e.*, greater than the typical margin of experimental error in repeat measurements of the same sample, expressed as one standard deviation from the mean of such measurements) in value of the level or profile signals a positive treatment outcome (*i.e.*, that administration of the agent has achieved a desired response). If the value for immune response does not change significantly, or decreases, a negative treatment outcome is indicated.

In other methods, a control value (*i.e.*, a mean and standard deviation) of level or profile is determined for a control population. Typically the individuals in the control population have not received prior treatment. Measured values of the level or profile in a patient after administering a therapeutic agent are then compared with the

control value. A significant increase relative to the control value (*e.g.*, greater than one standard deviation from the mean) signals a positive or sufficient treatment outcome. A lack of significant increase or a decrease signals a negative or insufficient treatment outcome. Administration of agent is generally continued while the level is increasing relative to the control value. As before, attainment of a plateau relative to control values is an indicator that the administration of treatment can be discontinued or reduced in dosage and/or frequency.

In other methods, a control value of the level or profile (*e.g.*, a mean and standard deviation) is determined from a control population of individuals who have undergone treatment with a therapeutic agent and whose levels or profiles have plateaued in response to treatment. Measured values of levels or profiles in a patient are compared with the control value. If the measured level in a patient is not significantly different (*e.g.*, more than one standard deviation) from the control value, treatment can be discontinued. If the level in a patient is significantly below the control value, continued administration of agent is warranted. If the level in the patient persists below the control value, then a change in treatment may be indicated.

In other methods, a patient who is not presently receiving treatment but has undergone a previous course of treatment is monitored for antibody levels or profiles to determine whether a resumption of treatment is required. The measured level or profile in the patient can be compared with a value previously achieved in the patient after a previous course of treatment. A significant decrease relative to the previous measurement (*i.e.*, greater than a typical margin of error in repeat measurements of the same sample) is an indication that treatment can be resumed. Alternatively, the value measured in a patient can be compared with a control value (mean plus standard deviation) determined in a population of patients after undergoing a course of treatment. Alternatively, the measured value in a patient can be compared with a control value in populations of prophylactically treated patients who remain free of symptoms of disease, or populations of therapeutically treated patients who show amelioration of disease characteristics. In all of these cases, a significant decrease relative to the control level (*i.e.*, more than a standard deviation) is an indicator that treatment should be resumed in a patient.

The tissue sample for analysis is typically blood, plasma, serum, mucous fluid or cerebrospinal fluid from the patient. The sample is analyzed, for example, for levels or profiles of antibodies to Aβ peptide, *e.g.*, levels or profiles of humanized antibodies. ELISA methods of detecting antibodies specific to Aβ are described in the Examples section. In some methods, the level or profile of an administered antibody is determined using a clearing assay, for example, in an *in vitro* phagocytosis assay, as described herein. In such methods, a tissue sample from a patient being tested is contacted with amyloid deposits (*e.g.*, from a PDAPP mouse) and phagocytic cells bearing Fc receptors. Subsequent clearing of the amyloid deposit is then monitored. The existence and extent of clearing response provides an indication of the existence and level of antibodies effective to clear Aβ in the tissue sample of the patient under test.

The antibody profile following passive immunization typically shows an immediate peak in antibody concentration followed by an exponential decay. Without a further dosage, the decay approaches pretreatment levels within a period of days to months depending on the half-life of the antibody administered. For example the half-life of some human antibodies is of the order of 20 days.

In some methods, a baseline measurement of antibody to Aβ in the patient is made before administration, a second measurement is made soon thereafter to determine the peak antibody level, and one or more further measurements are made at intervals to monitor decay of antibody levels. When the level of antibody has declined to baseline or a predetermined percentage of the peak less baseline *(e.g.*, 50%, 25% or 10%), administration of a further dosage of antibody is administered. In some methods, peak or subsequent measured levels less background are compared with reference levels previously determined to constitute a beneficial prophylactic or therapeutic treatment regime in other patients. If the measured antibody level is significantly less than a reference level (*e.g.*, less than the mean minus one standard deviation of the reference value in population of patients benefiting from treatment) administration of an additional dosage of antibody is indicated.

Additional methods include monitoring, over the course of treatment, any art-recognized physiologic symptom (*e.g.*, physical or mental symptom) routinely relied on by researchers or physicians to diagnose or monitor amyloidogenic diseases (*e.g.*, Alzheimer's disease). For example, one can monitor cognitive impairment. The latter

is a symptom of Alzheimer's disease and Down's syndrome but can also occur without other characteristics of either of these diseases. For example, cognitive impairment can be monitored by determining a patient's score on the Mini-Mental State Exam in accordance with convention throughout the course of treatment.

C. Kits

The invention further provides kits for performing the monitoring methods described above. Typically, such kits contain an agent that specifically binds to antibodies to Aβ. The kit can also include a label. For detection of antibodies to Aβ, the label is typically in the form of labeled anti-idiotypic antibodies. For detection of antibodies, the agent can be supplied prebound to a solid phase, such as to the wells of a microtiter dish. Kits also typically contain labeling providing directions for use of the kit. The labeling may also include a chart or other correspondence regime correlating levels of measured label with levels of antibodies to Aβ. The term labeling refers to any written or recorded material that is attached to, or otherwise accompanies a kit at any time during its manufacture, transport, sale or use. For example, the term labeling encompasses advertising leaflets and brochures, packaging materials, instructions, audio or videocassettes, computer discs, as well as writing imprinted directly on kits.

The invention also provides diagnostic kits, for example, research, detection and/or diagnostic kits (*e.g.*, for performing *in vivo* imaging). Such kits typically contain an antibody for binding to an epitope of Aβ, preferably within residues 1-10. Preferably, the antibody is labeled or a secondary labeling reagent is included in the kit. Preferably, the kit is labeled with instructions for performing the intended application, for example, for performing an *in vivo* imaging assay. Exemplary antibodies are those described herein.

D. *In vivo* Imaging

The invention provides methods of *in vivo* imaging amyloid deposits in a patient. Such methods are useful to diagnose or confirm diagnosis of Alzheimer's disease, or susceptibility thereto. For example, the methods can be used on a patient presenting with symptoms of dementia. If the patient has abnormal amyloid deposits, then the patient is likely suffering from Alzheimer's disease. The methods can also be

used on asymptomatic patients. Presence of abnormal deposits of amyloid indicates susceptibility to future symptomatic disease. The methods are also useful for monitoring disease progression and/or response to treatment in patients who have been previously diagnosed with Alzheimer's disease.

The methods work by administering a reagent, such as antibody that binds to Aβ, to the patient and then detecting the agent after it has bound. Preferred antibodies bind to Aβ deposits in a patient without binding to full length APP polypeptide. Antibodies binding to an epitope of Aβ within amino acids 1-10 are particularly preferred. In some methods, the antibody binds to an epitope within amino acids 7-10 of Aβ. Such antibodies typically bind without inducing a substantial clearing response. In other methods, the antibody binds to an epitope within amino acids 1-7 of Aβ. Such antibodies typically bind and induce a clearing response to Aβ. However, the clearing response can be avoided by using antibody fragments lacking a full-length constant region, such as Fabs. In some methods, the same antibody can serve as both a treatment and diagnostic reagent. In general, antibodies binding to epitopes C-terminal to residue 10 of Aβ do not show as strong a signal as antibodies binding to epitopes within residues 1-10, presumably because the C-terminal epitopes are inaccessible in amyloid deposits. Accordingly, such antibodies are less preferred.

Diagnostic reagents can be administered by intravenous injection into the body of the patient, or directly into the brain by intracranial injection or by drilling a hole through the skull. The dosage of reagent should be within the same ranges as for treatment methods. Typically, the reagent is labeled, although in some methods, the primary reagent with affinity for Aβ is unlabelled and a secondary labeling agent is used to bind to the primary reagent. The choice of label depends on the means of detection. For example, a fluorescent label is suitable for optical detection. Use of paramagnetic labels is suitable for tomographic detection without surgical intervention. Radioactive labels can also be detected using PET or SPECT.

Diagnosis is performed by comparing the number, size, and/or intensity of labeled loci, to corresponding baseline values. The base line values can represent the mean levels in a population of undiseased individuals. Baseline values can also represent previous levels determined in the same patient. For example, baseline values can be determined in a patient before beginning treatment, and measured values

thereafter compared with the baseline values. A decrease in values relative to baseline signals a positive response to treatment.

The present invention will be more fully described by the following non-limiting examples.

EXAMPLES

Example I. Therapeutic Efficacy of Anti-Aβ Antibodies: mAb 2H3, mAb 10D5, mAb 266, mAb 21F12 and pAb Aβ1-42

This example tests the capacity of various monoclonal and polyclonal antibodies to Aβ to inhibit accumulation of Aβ in the brain of heterozygotic transgenic mice.

A. Study Design

Sixty male and female, heterozygous PDAPP transgenic mice, 8.5 to 10.5 months of age were obtained from Charles River Laboratory. The mice were sorted into six groups to be treated with various antibodies directed to Aβ. Animals were distributed to match the gender, age, parentage and source of the animals within the groups as closely as possible. Table 2 depicts the Experimental design.

Table 2: Experimental Design

Treatment Group	N[a]	Treatment Antibody	Antibody Specificity	Antibody Isotype
1	9	none (PBS alone)	NA[b]	NA
2	10	Polyclonal	Aβ1-42	mixed
3	0	mAb[d] 2H3	Aβ1-12	IgG1
4	8	mAb 10D5	Aβ3-7	IgG1
5	6	mAb 266	Aβ13-28	IgG1
6	8	mAb 21F12	Aβ33-42	IgG2a

a. Number of mice in group at termination of the experiment. All groups started with 10 animals per group.
b. NA: not applicable
c. mouse polyclonal: anti-aggregated Aβ42
d. mAb: monoclonal antibody

As shown in Table 2, the antibodies included four murine Aβ-specific monoclonal antibodies, 2H3 (directed to Aβ residues 1-12), 10D5 (directed to Aβ residues 3-7), 266 (directed to Aβ residues 13-28 and binds to soluble but not to aggregated AN1792), 21F12 (directed to Aβ residues 33-42). A fifth group was treated with an Aβ-specific polyclonal antibody fraction (raised by immunization with aggregated AN1792). The negative control group received the diluent, PBS, alone without antibody.

B. Monitoring the Course of Treatment

The monoclonal antibodies were injected at a dose of about 10 mg/kg (assuming that the mice weighed 50 g). Antibody titers were monitored over the 28 weeks of treatment. Injections were administered intraperitoneally every seven days on average to maintain anti-Aβ titers above 1000. Although lower titers were measured for mAb 266 since it does not bind well to the aggregated AN1792 used as the capture antigen in the assay, the same dosing schedule was maintained for this group. The group

receiving monoclonal antibody 2H3 was discontinued within the first three weeks since the antibody was cleared too rapidly *in vivo*.

For determination of antibody titers, a subset of three randomly chosen mice from each group were bled just prior to each intraperitoneal inoculation, for a total of 30 bleeds. Antibody titers were measured as Aβ1-42-binding antibody using a sandwich ELISA with plastic multi-well plates coated with Aβ1-42 as described in detail in the General Materials and Methods. Mean titers for each bleed are set forth in Table 3 for the polyclonal antibody and the monoclonals 10D5 and 21F12.

Table 3:

weeks 21F12	21F12	weeks 10D5	10D5	weeks poly	poly
0.15	500	0.15	3000	0.15	1600
0.5	800	0.5	14000	0.5	4000
1	2500	1	5000	1	4500
1.5	1800	1.1	5000	1.5	3000
2	1400	1.2	1300	2	1300
3	6000	2	3000	3	1600
3.5	550	3	4000	3.5	650
4	1600	3.5	500	4	1300
5	925	4	2400	5	450
6	3300	5	925	6	2100
7	4000	6	1700	7	1300
8	1400	7	1600	8	2300
9	1900	8	4000	9	700
10	1700	9	1800	10	600
11	1600	10	1800	11	600
12	1000	11	2300	12	1000
13	1500	12	2100	13	900
14	1300	13	2800	14	1900
15	1000	14	1900	15	1200
16	1700	15	2700	16	700
17	1700	16	1300	17	2100
18	5000	17	2200	18	1800
19	900	18	2200	19	1800
20	300	19	2500	20	1200
22	1750	20	980	22	1000
23	1600	22	2000	23	1200
24	1000	23	1000	24	675
25	1100	24	850	25	850
26	2250	25	600	26	1600
27	1400	26	1100	27	1900
28		27	1450	28	
		28			

Titers averaged about 1000 over this time period for the polyclonal antibody preparation and were slightly above this level for the 10D5- and 21F12-treated animals.

Treatment was continued over a six-month period for a total of 196 days. Animals were euthanized one week after the final dose.

C. Aβ and APP Levels in the Brain:

Following about six months of treatment with the various anti-Aβ antibody preparations, brains were removed from the animals following saline perfusion. One hemisphere was prepared for immunohistochemical analysis and the second was used for the quantitation of Aβ and APP levels. To measure the concentrations of various forms of beta amyloid peptide and amyloid precursor protein (APP), the hemisphere was dissected and homogenates of the hippocampal, cortical, and cerebellar regions were prepared in 5M guanidine. These were serially diluted and the level of amyloid peptide or APP was quantitated by comparison to a series of dilutions of standards of Aβ peptide or APP of known concentrations in an ELISA format.

The levels of total Aβ and of Aβ1-42 measured by ELISA in homogenates of the cortex, and the hippocampus and the level of total Aβ in the cerebellum are shown in Tables 4, 5, and 6, respectively. The median concentration of total Aβ for the control group, inoculated with PBS, was 3.6-fold higher in the hippocampus than in the cortex (median of 63,389 ng/g hippocampal tissue compared to 17,818 ng/g for the cortex). The median level in the cerebellum of the control group (30.6 ng/g tissue) was more than 2,000-fold lower than in the hippocampus. These levels are similar to those previously reported for heterozygous PDAPP transgenic mice of this age (Johnson-Wood *et al.*, *supra*).

For the cortex, one treatment group had a median Aβ level, measured as Aβ1-42, which differed significantly from that of the control group ($p < 0.05$), those animals receiving the polyclonal anti-Aβ antibody as shown in Table 4. The median level of Aβ1-42 was reduced by 65%, compared to the control for this treatment group. The median levels of Aβ1-42 were also significantly reduced by 55% compared to the control in one additional treatment group, those animals dosed with the mAb 10D5 ($p = 0.0433$).

Table 4

CORTEX

Treatment Group	N[a]	Medians						Means	
		Total Aβ			Aβ42			Total Aβ	Aβ42
		ELISA value[b]	P value[c]	% Change	ELISA value	P value	% Change	ELISA value	ELISA value
PBS	9	17818	NA[d]	NA	13802	NA	NA	16150+/-7456[e]	12621+/-5738
Polyclonal anti-Aβ42	10	6160	0.0055	-65	4892	0.0071	-65	5912+/-4492	4454+/-3347
mAb 10D5	8	7915	0.1019	-56	6214	0.0433	-55	9695+/-6929	6943+/-3351
mAb 266	6	9144	0.1255	-49	8481	0.1255	-39	9204+/-9293	7489+/-6921
mAb 21F12	8	15158	0.2898	-15	13578	0.7003	-2	12481+/-7082	11005+/-6324

Footnotes:

a. Number of animals per group at the end of the experiment
b. ng/g tissue
c. Mann Whitney analysis
d. NA: not applicable
e. Standard Deviation

In the hippocampus, the median percent reduction of total Aβ associated with treatment with polyclonal anti-Aβ antibody (50%, $p = 0.0055$) was not as great as that observed in the cortex (65%) (Table 5). However, the absolute magnitude of the reduction was almost 3-fold greater in the hippocampus than in the cortex, a net reduction of 31,683 ng/g tissue in the hippocampus versus 11,658 ng/g tissue in the cortex. When measured as the level of the more amyloidogenic form of Aβ, Aβ1-42, rather than as total Aβ, the reduction achieved with the polyclonal antibody was significant ($p = 0.0025$). The median levels in groups treated with the mAbs 10D5 and 266 were reduced by 33% and 21%, respectively.

Table 5

HIPPOCAMPUS									
Treatment Group	N[a]	Medians						Means	
		Total Aβ			Aβ42			Total Aβ	Aβ42
		ELISA value[b]	P value[c]	% Change	ELISA value	P value	% Change	ELISA value	ELISA value
PBS	9	63389	NA[d]	NA	54429	NA	NA	58351+/-13308[e]	52801+/-14701
Polyclonal anti-Aβ42	10	31706	0.0055	-50	27127	0.0025	-50	30058+/-22454	24853+/-18262
mAb 10D5	8	46779	0.0675	-26	36290	0.0543	-33	44581+/-18632	36465+/-17146
mAb 266	6	48689	0.0990	-23	43034	0.0990	-21	36419+/-27304	32919+/-25372
mAb 21F12	8	51563	0.7728	-19	47961	0.8099	-12	57327+/-28927	50305+/-23927

a. Number of animals per group at the end of the experiment
b. ng/g tissue
c. Mann Whitney analysis
d. NA: not applicable
e. Standard Deviation

Total Aβ was also measured in the cerebellum (Table 6). Those groups dosed with the polyclonal anti-Aβ and the 266 antibody showed significant reductions of the levels of total Aβ (43% and 46%, p = 0.0033 and p = 0.0184, respectively) and that group treated with 10D5 had a near significant reduction (29%, p = 0.0675).

Table 6

CEREBELLUM					
Treatment Group	N[a]	Medians			Means
		Total Aβ			Total Aβ
		ELISA value[b]	P value[c]	% Change	ELISA value
PBS	9	30.64	NA[d]	NA	40.00+/-31.89[e]
Polyclonal anti-Aβ42	10	17.61	0.0033	-43	18.15+/-4.36
mAb 10D5	8	21.68	0.0675	-29	27.29+/-19.43
mAb 266	6	16.59	0.0184	-46	19.59+/-6.59
mAb 21F12	8	29.80	>0.9999	-3	32.88+/-9.90

a. Number of animals per group at the end of the experiment
b. ng/g tissue
c. Mann Whitney analysis
d. NA: not applicable
e. Standard Deviation

APP concentration was also determined by ELISA in the cortex and cerebellum from antibody-treated and control, PBS-treated mice. Two different APP assays were utilized. The first, designated APP-α/FL, recognizes both APP-alpha (α, the secreted form of APP which has been cleaved within the Aβ sequence), and full-length forms (FL) of APP, while the second recognizes only APP-α. In contrast to the treatment-associated diminution of Aβ in a subset of treatment groups, the levels of APP were virtually unchanged in all of the treated compared to the control animals. These

results indicate that the immunizations with Aβ antibodies deplete Aβ without depleting APP.

In summary, Aβ levels were significantly reduced in the cortex, hippocampus and cerebellum in animals treated with the polyclonal antibody raised against AN1792. To a lesser extent monoclonal antibodies to the amino terminal region of Aβ1-42, specifically amino acids 1-16 and 13-28 also showed significant treatment effects.

D. Histochemical Analyses:

The morphology of Aβ-immunoreactive plaques in subsets of brains from mice in the PBS, polyclonal Aß42, 21F12, 266 and 10D5 treatment groups was qualitatively compared to that of previous studies in which standard immunization procedures with Aβ42 were followed.

The largest alteration in both the extent and appearance of amyloid plaques occurred in the animals immunized with the polyclonal Aβ42 antibody. The reduction of amyloid load, eroded plaque morphology and cell-associated Aβ immunoreactivity closely resembled effects produced by the standard immunization procedure. These observations support the ELISA results in which significant reductions in both total Aβ and Aβ42 were achieved by administration of the polyclonal Aβ42 antibody.

In similar qualitative evaluations, amyloid plaques in the 10D5 group were also reduced in number and appearance, with some evidence of cell-associated Aβ immunoreactivity. Relative to control-treated animals, the polyclonal Ig fraction against Aβ and one of the monoclonal antibodies (10D5) reduced plaque burden by 93% and 81%, respectively ($p<0.005$). 21F12 appeared to have a relatively modest effect on plaque burden. Micrographs of brain after treatment with pAbAβ_{1-42} show diffuse deposits and absence of many of the larger compacted plaques in the pAbAβ_{1-42} treated group relative to control treated animals.

E. Lymphoproliferative Responses

Aβ-dependent lymphoproliferation was measured using spleen cells harvested eight days following the final antibody infusion. Freshly harvested cells, 10^5

per well, were cultured for 5 days in the presence of Aβ1-40 at a concentration of 5 μM for stimulation. As a positive control, additional cells were cultured with the T cell mitogen, PHA, and, as a negative control, cells were cultured without added peptide.

Splenocytes from aged PDAPP mice passively immunized with various anti-Aβ antibodies were stimulated *in vitro* with AN1792 and proliferative and cytokine responses were measured. The purpose of these assays was to determine if passive immunization facilitated antigen presentation, and thus priming of T cell responses specific for AN1792. No AN1792-specific proliferative or cytokine responses were observed in mice passively immunized with the anti-Aβ antibodies.

Example II: Therapeutic Efficacy of Anti-Aβ Antibodies: mAb 2H3, mAb 10D5, mAb 266, mAb 21F12, mAb 3D6, mAb 16C11 and pAb Aβ1-42

In a second study, treatment with 10D5 was repeated and two additional anti-Aβ antibodies were tested, monoclonals 3D6 (Aβ1-5) and 16C11 (Aβ33-42). Control groups received either PBS or an irrelevant isotype-matched antibody (TM2a). The mice were older (11.5-12 month old heterozygotes) than in the previous study, otherwise the experimental design was the same. Once again, after six months of treatment, 10D5 reduced plaque burden by greater than 80% relative to either the PBS or isotype-matched antibody controls (p=0.003). One of the other antibodies against Aβ, 3D6, was equally effective, producing an 86% reduction (p=0.003). In contrast, the third antibody against the peptide, 16C11, failed to have any effect on plaque burden. Similar findings were obtained with Aβ42 ELISA measurements.

These results demonstrate that an antibody response against Aβ peptide, in the absence of T cell immunity, is sufficient to decrease amyloid deposition in PDAPP mice, but that not all anti-Aβ antibodies are equally efficacious. Antibodies directed to epitopes comprising amino acids 1-5 or 3-7 of Aβ are particularly efficacious. In summary, it can be demonstrated that passively administered antibodies against Aβ (*i.e.*, passive immunization) reduces the extent of plaque deposition in a mouse model of Alzheimer's disease.

<u>Example III: Monitoring of Antibody Binding in the CNS</u>

This Example demonstrates that when held at modest serum concentrations (25–70 μg/ml), the antibodies gained access to the CNS at levels sufficient to decorate β-amyloid plaques.

To determine whether antibodies against Aβ could be acting directly within the CNS, brains taken from saline-perfused mice at the end of the Example II, were examined for the presence of the peripherally-administered antibodies. Unfixed cryostat brain sections were exposed to a fluorescent reagent against mouse immunoglobulin (goat anti-mouse IgG-Cy3). Plaques within brains of the 10D5 and 3D6 groups were strongly decorated with antibody, while there was no staining in the 16C11 group. To reveal the full extent of plaque deposition, serial sections of each brain were first immunoreacted with an anti-Aβ antibody, and then with the secondary reagent. 10D5 and 3D6, following peripheral administration, gained access to most plaques within the CNS. The plaque burden was greatly reduced in these treatment groups compared to the 16C11 group. Antibody entry into the CNS was not due to abnormal leakage of the blood-brain barrier since there was no increase in vascular permeability as measured by Evans Blue in PDAPP mice. In addition, the concentration of antibody in the brain parenchyma of aged PDAPP mice was the same as in non-transgenic mice, representing 0.1% of the antibody concentration in serum (regardless of isotype).

These data indicate that peripherally administered antibodies can enter the CNS where they can directly trigger amyloid clearance. It is likely that 16C11 also had access to the plaques but was unable to bind.

<u>Example IV: *Ex vivo* Screening Assay for Activity of an Antibody Against Amyloid Deposits</u>

To examine the effect of antibodies on plaque clearance, we established an *ex vivo* assay in which primary microglial cells were cultured with unfixed cryostat sections of either PDAPP mouse or human AD brains. Microglial cells were obtained from the cerebral cortices of neonate DBA/2N mice (1-3 days). The cortices were mechanically dissociated in HBSS^{--} (Hanks' Balanced Salt Solution, Sigma) with 50 μg/ml DNase I (Sigma). The dissociated cells were filtered with a 100 μm cell strainer

(Falcon), and centrifuged at 1000 rpm for 5 minutes. The pellet was resuspended in growth medium (high glucose DMEM, 10%FBS, 25ng/ml rmGM-CSF), and the cells were plated at a density of 2 brains per T-75 plastic culture flask. After 7-9 days, the flasks were rotated on an orbital shaker at 200 rpm for 2h at 37°C. The cell suspension was centrifuged at 1000rpm and resuspended in the assay medium.

10-μm cryostat sections of PDAPP mouse or human AD brains (post-mortem interval < 3hr) were thaw mounted onto poly-lysine coated round glass coverslips and placed in wells of 24-well tissue culture plates. The coverslips were washed twice with assay medium consisting of H-SFM (Hybridoma-serum free medium, Gibco BRL) with 1% FBS, glutamine, penicillin/streptomycin, and 5ng/ml rmGM-CSF (R&D). Control or anti-Aβ antibodies were added at a 2x concentration (5 μg/ml final) for 1 hour. The microglial cells were then seeded at a density of 0.8x 10^6 cells/ml assay medium. The cultures were maintained in a humidified incubator (37°C, 5%CO_2) for 24hr or more. At the end of the incubation, the cultures were fixed with 4% paraformaldehyde and permeabilized with 0.1% Triton-X100. The sections were stained with biotinylated 3D6 followed by a streptavidin / Cy3 conjugate (Jackson ImmunoResearch). The exogenous microglial cells were visualized by a nuclear stain (DAPI). The cultures were observed with an inverted fluorescent microscope (Nikon, TE300) and photomicrographs were taken with a SPOT digital camera using SPOT software (Diagnostic instruments). For Western blot analysis, the cultures were extracted in 8M urea, diluted 1:1 in reducing tricine sample buffer and loaded onto a 16% tricine gel (Novex). After transfer onto immobilon, blots were exposed to 5 μg/ml of the pabAβ42 followed by an HRP-conjugated anti-mouse antibody, and developed with ECL (Amersham)

When the assay was performed with PDAPP brain sections in the presence of 16C11 (one of the antibodies against Aβ that was not efficacious *in vivo*), β-amyloid plaques remained intact and no phagocytosis was observed. In contrast, when adjacent sections were cultured in the presence of 10D5, the amyloid deposits were largely gone and the microglial cells showed numerous phagocytic vesicles containing Aβ. Identical results were obtained with AD brain sections; 10D5 induced phagocytosis of AD plaques, while 16C11 was ineffective. In addition, the assay provided

comparable results when performed with either mouse or human microglial cells, and with mouse, rabbit, or primate antibodies against Aβ.

Table 7 compares Aβ binding versus phagocytosis for several different antibody binding specificities. It can be seen that antibodies binding to epitopes within aa 1-7 both bind and clear amyloid deposits, whereas antibodies binding to epitopes within amino acids 4-10 bind without clearing amyloid deposits. Antibodies binding to epitopes C-terminal to residue 10 neither bind nor clear amyloid deposits.

Table 7: Analysis of Epitope Specificity

	Antibody			
	epitope	**isotype**	**Staining**	**Phagocytosis**
N-Term				
mab				
3D6	1-5	IgG2b	+	+
10D5	3-7	IgG1	+	+
22C8	3-7	IgG2a	+	+
6E10	5-10	IgG1	+	-
14A8	4-10	rat IgG1	+	-
aa 13-28				
18G11	10-18	rat IgG1	-	-
266	16-24	IgG1	-	-
22D12	18-21	IgG2b	-	-
C-Term				
2G3	-40	IgG1	-	-
16C11	-40/-42	IgG1	-	-
21F12	-42	IgG2a	-	-
Immune serum				
rabbit (CFA)	1-6		+	+
mouse (CFA)	3-7		+	+
mouse (QS-21)	3-7		+	+
monkey (QS-21)	1-5		+	+
mouse (MAP1-7)			+	+

Table 8 shows results obtained with several antibodies against Aβ, comparing their abilities to induce phagocytosis in the *ex vivo* assay and to reduce *in vivo* plaque burden in passive transfer studies. Although 16C11 and 21F12 bound to aggregated synthetic Aβ peptide with high avidity, these antibodies were unable to react with β-amyloid plaques in unfixed brain sections, could not trigger phagocytosis in the *ex vivo* assay, and were not efficacious *in vivo*. 10D5, 3D6, and the polyclonal antibody against Aβ were active by all three measures. These results show that efficacy *in vivo* is due to direct antibody mediated clearance of the plaques within the CNS, and that the *ex vivo* assay is predictive of *in vivo* efficacy.

Table 8: The *ex vivo* assay as predictor of *in vivo* efficacy

Antibody	**Isotype**	**Avidity for aggregated Aβ (pM)**	**Binding to β-amyloid plaques**	***Ex vivo* efficacy**	***In vivo* efficacy**
monoclonal					
3D6	IgG2b	470	+	+	+
10D5	IgG1	43	+	+	+
16C11	IgG1	90	-	-	-
21F12	IgG2a	500	-	-	-
TM2a	IgG1	-	-	-	-
polyclonal					
1-42	mix	600	+	+	+

The same assay has been used to test clearing activity of an antibody against a fragment of synuclein referred to as NAC. Synuclein has been shown to be an amyloid plaque-associated protein. An antibody to NAC was contacted with a brain tissue sample containing amyloid plaques, and microglial cells, as before. Rabbit serum was used as a control. Subsequent monitoring showed a marked reduction in the number and size of plaques indicative of clearing activity of the antibody.

Confocal microscopy was used to confirm that Aβ was internalized during the course of the *ex vivo* assay. In the presence of control antibodies, the exogenous microglial cells remained in a confocal plane above the tissue, there were no phagocytic vesicles containing Aβ, and the plaques remained intact within the section.

In the presence of 10D5, nearly all plaque material was contained in vesicles within the exogenous microglial cells. To determine the fate of the internalized peptide, 10D5 treated cultures were extracted with 8M urea at various time-points, and examined by Western blot analysis. At the one hour time point, when no phagocytosis had yet occurred, reaction with a polyclonal antibody against Aβ revealed a strong 4 kD band (corresponding to the Aβ peptide). Aβ immunoreactivity decreased at day 1 and was absent by day 3. Thus, antibody-mediated phagocytosis of Aβ leads to its degradation.

To determine if phagocytosis in the *ex vivo* assay was Fc-mediated, F(ab')2 fragments of the anti-Aß antibody 3D6 were prepared. Although the F(ab')2 fragments retained their full ability to react with plaques, they were unable to trigger phagocytosis by microglial cells. In addition, phagocytosis with the whole antibody could be blocked by a reagent against murine Fc receptors (anti-CD16/32). These data indicate that *in vivo* clearance of Aβ occurs through Fc-receptor mediated phagocytosis.

<u>Example V: Passage of Antibodies Through the Blood-Brain Barrier</u>

This example determines the concentration of antibody delivered to the brain following intravenous injection into a peripheral tissue of either normal or PDAPP mice. Following treatment, PDAPP or control normal mice were perfused with 0.9% NaCl. Brain regions (hippocampus or cortex) were dissected and rapidly frozen. Brain were homogenized in 0.1% triton + protease inhibitors. Immunoglobulin was detected in the extracts by ELISA. F(ab)'2 goat anti-mouse IgG were coated onto an RIA plate as capture reagent. The serum or the brain extracts were incubated for 1hr. The isotypes were detected with anti-mouse IgG1-HRP or IgG2a-HRP or IgG2b-HRP (Caltag). Antibodies, regardless of isotype, were present in the CNS at a concentration that is 1:1000 that found in the blood. For example, when the concentration of IgG1 was three times that of IgG2a in the blood, it was three times IgG2a in the brain as well, both being present at 0.1% of their respective levels in the blood. This result was observed in both transgenic and nontransgenic mice indicating that the PDAPP does not have a uniquely leak blood brain barrier.

Example VI. Cloning and Sequencing of the Mouse 3D6 Variable Regions

Cloning and Sequence Analysis of 3D6 VH. The heavy chain variable VH region of 3D6 was cloned by RT-PCR using mRNA prepared from hybridoma cells by two independent methods. In the first, consensus primers were employed to VH region leader peptide encompassing the translation initiation codon as the 5' primer (DNA #3818-3829), and a g2b (DNA #3832) constant regions specific 3' primer. The sequences from PCR amplified product, as well as from multiple, independently-derived clones, were in complete agreement with one another. As a further check on the sequence of the 3D6 VH region, the result was confirmed by sequencing a VH fragment obtained by 5' RACE RT-PCR methodology and the 3' g2b specific primer (DNA #3832). Again, the sequence was derived from the PCR product, as well as multiple, independently-isolated clones. Both sequences are in complete agreement with one another, (with the exception of V8I substitution in the leader region from the 5' RACE product), indicating that the sequences are derived from the mRNA encoding the VH region of 3D6. The nucleotide (SEQ ID NO:3) and amino acid sequence (SEQ ID NO:4) of the VH region of 3D6 are set forth in Table 9A and in Figure 2, respectively.

Table 9A: Mouse 3D6 VH Nucleotide Sequence

<u>ATGAACTTCGGGCTCAGCTTGATTTTCCTTGTCCTTGTTTTAAAAGGTGTCCAGTGT</u>GA
AGTGAAGCTGGTGGAGTCTGGGGGAGGCTTAGTGAAGCCTGGAGCGTCTCTGAAACTCT
CCTGTGCAGCCTCTGGATTCACTTTCAGTAACTATGGCATGTCTTGGGTTCGCCAGAAT
TCAGACAAGAGGCTGGAGTGGGTTGCATCCATTAGGAGTGGTGGTGGTAGAACCTACTA
TTCAGACAATGTAAAGGGCCGATTCACCATCTCCAGAGAGAATGCCAAGAACACCCTGT
ACCTGCAAATGAGTAGTCTGAAGTCTGAGGACACGGCCTTGTATTATTGTGTCAGATAT
GATCACTATAGTGGTAGCTCCGACTACTGGGGCCAGGGCACCACT (SEQ ID NO:3)

*Leader peptide is underlined.

Cloning and Sequence Analysis of 3D6 VL. The light chain variable VL region of 3D6 was cloned in an analogous manner as the VH region. In the first trial, a consensus primer set was designed for amplification of murine VL regions as follows: 5' primers (DNA #3806-3816) were designed to hybridize to the VL region encompassing the translation initiation codon, and a 3' primer (DNA#3817) was specific

for the murine Ck region downstream of the V-J joining region. DNA sequence analysis of the PCR fragment, as well as independently-derived clones isolated using this consensus light chain primer set, revealed that the cDNA obtained was derived from a non-functionally rearranged message as the sequence contained a frameshift mutation between the V-J region junction.

In a second trial, 5'RACE was employed to clone a second VL encoding cDNA. DNA sequence analysis of this product (consensus 11) showed it encoded a functional mRNA. Thus, it can be concluded that the sequence encodes the correct 3D6 light chain mRNA. The nucleotide (SEQ ID NO:1) and amino acid sequence (SEQ ID NO:2) of the VL region of 3D6 are set forth in Table 9B and in Figure 1, respectively.

Table 9B: Mouse 3D6 VL Nucleotide Sequence

ATGATGAGTCCTGCCCAGTTCCTGTTTCTGTTAGTGCTCTGGATTCGGGAAACCAACGG
TTATGTTGTGATGACCCAGACTCCACTCACTTTGTCGGTTACCATTGGACAACCAGCCT
CCATCTCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTGATGGAAAGACATATTTGAAT
TGGTTGTTACAGAGGCCAGGCCAGTCTCCAAAGCGCCTAATCTATCTGGTGTCTAAACT
GGACTCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTTACACTGA
AAATCAGCAGAATAGAGGCTGAGGATTTGGGACTTTATTATTGCTGGCAAGGTACACAT
TTTCCTCGGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAA (SEQ ID NO:1)

*Leader peptide is underlined

Primers used for the cloning of the 3D6 VL cDNA are set forth in Table 10.

DNA	Size	Coding Strand?	DNA Sequence	Comments
3806	40	Yes	ACT.AGT.CGA.CAT.GAA.GTT.GCC.TGT.TAG.GCT.GTT.GGT.GCT.G (SEQ ID NO:39)	mouse kappa variable primer 1 MKV PRIMER 1, MRC set; % A+T = 50.00 [20]; % C+G = 50.00 [20] Davis,Botstein,Roth Melting Temp C. 72.90

3807	39	Yes	ACT.AGT.CGA.CAT.GGA.GWC.AGA.CAC.ACT.CCT.GYT.ATG.GGT (SEQ ID NO:40)	mouse kappa variable primer 2 MKV PRIMER 2, MRC set % A+T = 46.15 [18]; % C+G = 48.72 [19] Davis,Botstein,Roth Melting Temp C. 72.05
3808	40	Yes	ACT.AGT.CGA.CAT.GAG.TGT.GCT.CAC.TCA.GGT.CCT.GGS.GTT.G (SEQ ID NO:41)	mouse kappa variable primer 3 MKV PRIMER 3, MRC set; % A+T = 45.00 [18]; % C+G = 52.50 [21] Davis,Botstein,Roth Melting Temp C. 73.93
3809	43	Yes	ACT.AGT.CGA.CAT.GAG.GRC.CCC.TGC.TCA.GWT.TYT.TGG.MWT.CTT.G (SEQ ID NO:42)	mouse kappa variable primer 4 MKV PRIMER 4, MRC set; % A+T = 41.86 [18]; % C+G = 46.51 [20] Davis,Botstein,Roth Melting Temp C. 72.34
3810	40	Yes	ACT.AGT.CGA.CAT.GGA.TTT.WCA.GGT.GCA.GAT.TWT.CAG.CTT.C (SEQ ID NO:43)	mouse kappa variable primer 5 MKV PRIMER 5, MRC set % A+T = 52.50 [21]; % C+G = 42.50 [17] Davis,Botstein,Roth Melting Temp C. 69.83
3811	37	Yes	ACT.AGT.CGA.CAT.GAG.GTK.CYY.TGY.TSA.GYT.YCT.GRG.G (SEQ ID NO:44)	mouse kappa variable primer 6 MKV PRIMER 6, MRC set; % A+T = 37.84 [14]; % C+G = 40.54 [15] Davis,Botstein,Roth Melting Temp C. 68.01
3812	41	Yes	ACT.AGT.CGA.CAT.GGG.CWT.CAA.GAT.GGA.GTC.ACA.KWY.YCW.GG (SEQ ID NO:45)	mouse kappa variable primer 7 MKV PRIMER 7, MRC set; % A+T = 39.02 [16]; % C+G = 46.34 [19] Davis,Botstein,Roth Melting Temp C. 71.70
3813	41	Yes	ACT.AGT.CGA.CAT.GTG.GGG.AYC.TKT.TTY.CMM.TTT.TTC.AAT.TG (SEQ ID NO:46)	mouse kappa variable primer 8 MKV PRIMER 8, MRC set; % A+T = 53.66 [22]; % C+G = 34.15 [14] Davis,Botstein,Roth Melting Temp C. 66.70

3814	35	Yes	ACT.AGT.CGA.CAT.GGT.RTC.CWC.ASC.TCA.GTT.CCT.TG (SEQ ID NO:47)	mouse kappa variable primer 9 MKV PRIMER 9, MRC set. % A+T = 45.71 [16]; % C+G = 45.71 [16] Davis,Botstein,Roth Melting Temp C. 69.36
3815	37	Yes	ACT.AGT.CGA.CAT.GTA.TAT.ATG.TTT.GTT.GTC.TAT.TTC.T (SEQ ID NO:48)	mouse kappa variable primer 10 MKV PRIMER 10, MRC set; % A+T = 70.27 [26]; % C+G = 29.73 [11] Davis,Botstein,Roth Melting Temp C. 63.58
3816	38	Yes	ACT.AGT.CGA.CAT.GGA.AGC.CCC.AGC.TCA.GCT.TCT.CTT.CC (SEQ ID NO:49)	mouse kappa variable primer 11 MKV PRIMER 11, MRC set; % A+T = 44.74 [17]; % C+G = 55.26 [21] Davis,Botstein,Roth Melting Temp C. 74.40
3817	27	No	GGA.TCC.CGG.GTG.GAT.GGT.GGG.AAG.ATG (SEQ ID NO:50)	mouse kappa light chain reverse primer, aa 116-122; Ck constant region primer, MRC set+SmaI site; % A+T = 47.06 [8]; % C+G = 52.94 [9] Davis,Botstein,Roth Melting Temp C. 57.19
3818	37	Yes	ACT.AGT.CGA.CAT.GAA.ATG.CAG.CTG.GGT.CAT.STT.CTT.C (SEQ ID NO:51)	mouse heavy variable primer 1 MHV primer 1, MRC set;
3819	36	Yes	ACT.AGT.CGA.CAT.GGG.ATG.GAG.CTR.TAT.CAT.SYT.CTT (SEQ ID NO:52)	mouse heavy variable primer 2 MHV primer 2, MRC set;
3820	37	Yes	ACT.AGT.CGA.CAT.GAA.GWT.GTG.GTT.AAA.CTG.GGT.TTT.T (SEQ ID NO:53)	mouse heavy variable primer 3 MHV primer 3, MRC set;
3821	35	Yes	ACT.AGT.CGA.CAT.GRA.CTT.TGG.GYT.CAG.CTT.GRT.TT (SEQ ID NO:54)	mouse heavy variable primer 4 MHV primer 4, MRC set;
3822	40	Yes	ACT.AGT.CGA.CAT.GGA.CTC.CAG.GCT.CAA.TTT.AGT.TTT.CCT.T (SEQ ID NO:55)	mouse heavy variable primer 5 MHV primer 5, MRC set;

3823	37	Yes	ACT.AGT.CGA.CAT.GGC.TGT.CYT.RGS.GCT.RCT.CTT.CTG.C (SEQ ID NO:56)	mouse heavy variable primer 6 MHV primer 6, MRC set;
3824	36	Yes	ACT.AGT.CGA.CAT.GGR.ATG.GAG.CKG.GRT.CTT.TMT.CTT (SEQ ID NO:57)	mouse heavy variable primer 7 MHV primer 7, MRC set;
3825	33	Yes	ACT.AGT.CGA.CAT.GAG.AGT.GCT.GAT.TCT.TTT.GTG (SEQ ID NO:58)	mouse heavy variable primer 8 MHV primer 8, MRC set;
3826	40	Yes	ACT.AGT.CGA.CAT.GGM.TTG.GGT.GTG.GAM.CTT.GCT.ATT.CCT.G (SEQ ID NO:59)	mouse heavy variable primer 9 MHV primer 9, MRC set;
3827	37	Yes	ACT.AGT.CGA.CAT.GGG.CAG.ACT.TAC.ATT.CTC.ATT.CCT.G (SEQ ID NO:60)	mouse heavy variable primer 10 MHV primer 10, MRC set;
3828	38	Yes	ACT.AGT.CGA.CAT.GGA.TTT.TGG.GCT.GAT.TTT.TTT.TAT.TG (SEQ ID NO:61)	mouse heavy variable primer 11 MHV primer 11, MRC set;
3829	37	Yes	ACT.AGT.CGA.CAT.GAT.GGT.GTT.AAG.TCT.TCT.GTA.CCT.G (SEQ ID NO:62)	mouse heavy variable primer 12 MHV primer 12, MRC set;
3832	27	No	GGA.TCC.CGG.GAG.TGG.ATA.GAC.tGA.TGG (SEQ ID NO:63)	mouse IgG2b heavy chain reverse primer aa position 119-124, MRC set;

From N-terminal to C-terminal, both light and heavy chains comprise the domains FR1, CDR1, FR2, CDR2, FR3, CDR3 and FR4. The assignment of amino acids to each domain is in accordance with the numbering convention of Kabat *et al.*, *supra*.

Expression of Chimeric 3D6 Antibody: The variable heavy and light chain regions were re-engineered to encode splice donor sequences downstream of the respective VDJ or VJ junctions, and cloned into the mammalian expression vector pCMV-hγ1 for the heavy chain, and pCMV-hκ1 for the light chain. These vectors encode human γ1 and Ck constant regions as exonic fragments downstream of the

inserted variable region cassette. Following sequence verification, the heavy chain and light chain expression vectors were co-transfected into COS cells. Two different heavy chain clones (H2.2 & H3.2) were independently co-transfected with 3 different chimeric light chain clones (L3, L4, &L10) to confirm reproducibility of the result. A chimeric 21.6 antibody transfection was carried out as a positive control for the vectors. Conditioned media was collected 48 hrs post transfection and assayed by western blot analysis for antibody production or ELISA for Aβ binding.

The multiple transfectants all expressed heavy chain + light chain combinations which are recognized by a goat anti-human IgG (H+L) antibody on a western blot.

Direct binding of 3D6 and chimeric 3D6 (PK1614) antibodies to Aβ was tested by ELISA analysis. Chimeric 3D6 was found to bind to Aβ with high avidity, similar to that demonstrated by 3D6 (Figure 3A). Furthermore, an ELISA based competitive inhibition assay revealed that the chimeric 3D6 and the murine 3D6 antibody competed equally with biotinylated-3D6 binding to Aβ (Figure 3B). The chimeric antibody displayed binding properties indistinguishable from the 3D6 reference sample.

Table 11.

Conc (μg/ml)	3D6	PK1614	IgG1
0.037		119.3	
0.11	118.6	118.9	
0.33	99.7	71.25	
1	98.63	84.53	134.4

Moreover, both 3D6 and PK1614 were effective at clearing Aβ plaques. The *ex vivo* assay demonstrates that as the concentration of antibody increases, the amount of Aβ decreases in a similar manner for both murine and chimeric 3D6 antibodies. Hence, it can be concluded that the sequences encode functional 3D6 heavy chain and light chains respectively.

Example VII. 3D6 Humanization

Homology/Molecular Modeling. In order to identify key structural framework residues in the murine 3D6 antibody, a three-dimensional model was

generated based on the closest murine antibodies for the heavy and light chains. For this purpose, an antibody designated 1CR9 was chosen as a template for modeling the 3D6 light chain (PDB ID: 1CR9, Kanyo *et al., supra*), and an antibody designated 1OPG was chosen as the template for modeling the heavy chain. (PDB ID: 1OPG Kodandapani *et al., supra*). (See also Table 1.) Amino acid sequence alignment of 3D6 with the light chain and heavy chain of these antibodies revealed that, with the exception of CDR3 of the heavy chain, the 1CR9 and 1OPG antibodies share significant sequence homology with 3D6. In addition, the CDR loops of the selected antibodies fall into the same canonical Chothia structural classes as do the CDR loops of 3D6, again excepting CDR3 of the heavy chain. Therefore, 1CR9 and 1OPG were initially selected as antibodies of solved structure for homology modeling of 3D6.

A first pass homology model of 3D6 variable region based on the antibodies noted above was constructed using the Look & SegMod Modules GeneMine (v3.5) software package. This software was purchased under a perpetual license from Molecular Applications Group (Palo Alto, CA). This software package, authored by Drs. Michael Levitt and Chris Lee, facilitates the process of molecular modeling by automating the steps involved in structural modeling a primary sequence on a template of known structure based on sequence homology. Working on a Silicon Graphics IRIS workstation under a UNIX environment, the modeled structure is automatically refined by a series of energy minimization steps to relieve unfavorable atomic contacts and optimize electrostatic and van der Walls interactions.

A further refined model was built using the modeling capability of Quanta®. A query of the PDB database with CDR3 of the heavy chain of 3D6 identified 1qkz as most homologous and having the identical number of residues as 3D6. Hence, CDR3 of the heavy chain of 3D6 was modeled using the crystal structure of 1qkz as template. The α-carbon backbone trace of the 3D6 model is shown in Figure 4. The VH domain is shown as a stippled line, and VL domain is shown as a solid line, and CDR loops are indicated in ribbon form.

Selection of Human Acceptor Antibody Sequences. Suitable human acceptor antibody sequences were identified by computer comparisons of the amino acid sequences of the mouse variable regions with the sequences of known human antibodies. The comparison was performed separately for the 3D6 heavy and light chains. In

particular, variable domains from human antibodies whose framework sequences exhibited a high degree of sequence identity with the murine VL and VH framework regions were identified by query of the Kabat Database using NCBI BLAST (publicly accessible through the National Institutes of Health NCBI internet server) with the respective murine framework sequences.

Two candidate sequences were chosen as acceptor sequences based on the following criteria: (1) homology with the subject sequence; (2) sharing canonical CDR structures with the donor sequence; and (3) not containing any rare amino acid residues in the framework regions. The selected acceptor sequence for VL is Kabat ID Number (KABID) 019230 (Genbank Accession No. S40342), and for VH is KABID 045919 (Genbank Accession No. AF115110). First versions of humanized 3D6 antibody utilize these selected acceptor antibody sequences.

Substitution of Amino Acid Residues. As noted *supra*, the humanized antibodies of the invention comprise variable framework regions substantially from a human immunoglobulin (acceptor immunoglobulin) and complementarity determining regions substantially from a mouse immunoglobulin (donor immunoglobulin) termed 3D6. Having identified the complementarity determining regions of 3D6 and appropriate human acceptor immunoglobulins, the next step was to determine which, if any, residues from these components to substitute to optimize the properties of the resulting humanized antibody. The criteria described *supra* were used to select residues for substitution.

Figures 1 and 2 depict alignments of the original murine 3D6 VL and VH, respectively, with the respective version 1 of the humanized sequence, the corresponding human framework acceptor sequence and, lastly, the human germline V region sequence showing highest homology to the human framework acceptor sequence. The shaded residues indicate the canonical (solid fill), vernier (dotted outline), packing (bold), and rare amino acids (bold italics), and are indicated on the figure. The asterisks indicate residues backmutated to murine residues in the human acceptor framework sequence, and CDR regions are shown overlined. A summary of the changes incorporated into version 1 of humanized 3D6 VH and VL is presented in Table 12.

Table 12. Summary of changes in humanized 3D6.v1

Changes	VL (112 residues)	VH (119 residues)
Hu->Mu: Framework	4/112	3/119 (1 canon, 1 packing)
CDR1	6/16	3/5
CDR2	4/7	7/14
CDR3	5/8	4/10
Hu->Mu	19/112 (17%)	17/119 (14%)
Mu->Hu: Framework	13/112	14/119
Backmutation notes	1. I2V which is a canonical position. 2. Y36L which is a packing residue and also lies under the CDRs 3. L46R which is a packing residue and lies beneath the CDRs	4. S49A Vernier/beneath the CDRs. 5. A93V which is a packing and vernier zone residue 6. K94R which is a canonical residue
Acceptor notes	7. KABID 019230/Genbank Acc#S40342 8. Hu κ LC subgroup II 9. CDRs from same canonical structural group as donor (m3D6) L1=class 4 L2=class 1 L3=class1 10. Unknown specificity	11. KABID045919/Genbank Acc#AF115110 12. Hu HC subgroup III 13. CDRs from same canonical structural group as donor (m3D6) H1=class 1 H2=class3 14. Recognizes capsular polysaccharide of Neisseria meningitidis
Acceptor Germline	15. VH3-23	16. A3 & A19

Tables 13 and 14 set forth Kabat numbering keys for the various light and heavy chains, respectively.

Table 13: Key to Kabat Numbering for Light Chain

KAB #	#	TYPE	mouse 3D6 VL	HUM 3D6VL	KABID 019230	A19-Germ-line	Comment
1	1	FR1	Y	Y	D	D	Rare mouse, may contact CDR
2	2		V	V	I	I	Canonical/CDR contact
3	3		V	V	V	V	
4	4		M	M	M	M	
5	5		T	T	T	T	
6	6		Q	Q	Q	Q	
7	7		T	S	S	S	
8	8		P	P	P	P	
9	9		L	L	L	L	
10	10		T	S	S	S	
11	11		L	L	L	L	
12	12		S	P	P	P	
13	13		V	V	V	V	
14	14		T	T	T	T	
15	15		I	P	P	P	
16	16		G	G	G	G	
17	17		Q	E	E	E	
18	18		P	P	P	P	
19	19		A	A	A	A	
20	20		S	S	S	S	
21	21		I	I	I	I	
22	22		S	S	S	S	
23	23		C	C	C	C	

24	24	CDR1	K	K	R	R	
25	25		S	S	S	S	
26	26		S	S	S	S	
27	27		Q	Q	Q	Q	
27A	28		S	S	S	S	
27B	29		L	L	L	L	
27C	30		L	L	L	L	
27D	31		D	D	H	H	
27E	32		S	S	S	S	
28	33		D	D	N	N	
29	34		G	G	G	G	
30	35		K	K	Y	Y	
31	36		T	T	N	N	
32	37		Y	Y	Y	Y	
33	38		L	L	L	L	
34	39		N	N	D	D	
35	40	FR2	W	W	W	W	
36	41		L	L	Y	Y	Packing residue
37	42		L	L	L	L	
38	43		Q	Q	Q	Q	
39	44		R	K	K	K	
40	45		P	P	P	P	
41	46		G	G	G	G	
42	47		Q	Q	Q	Q	
43	48		S	S	S	S	
44	49		P	P	P	P	
45	50		K	Q	Q	Q	
46	51		R	R	L	L	Packing residue
47	52		L	L	L	L	
48	53		I	I	I	I	
49	54		Y	Y	Y	Y	
50	55	CDR2	L	L	L	L	
51	56		V	V	G	G	
52	57		S	S	S	S	
53	58		K	K	N	N	
54	59		L	L	R	R	
55	60		D	D	A	A	
56	61		S	S	S	S	

57	62	FR3	G	G	G	G
58	63		V	V	V	V
59	64		P	P	P	P
60	65		D	D	D	D
61	66		R	R	R	R
62	67		F	F	F	F
63	68		T	S	S	S
64	69		G	G	G	G
65	70		S	S	S	S
66	71		G	G	G	G
67	72		S	S	S	S
68	73		G	G	G	G
69	74		T	T	T	T
70	75		D	D	D	D
71	76		F	F	F	F
72	77		T	T	T	T
73	78		L	L	L	L
74	79		K	K	K	K
75	80		I	I	I	I
76	81		S	S	S	S
77	82		R	R	R	R
78	83		I	V	V	V
79	84		E	E	E	E
80	85		A	A	A	A
81	86		E	E	E	E
82	87		D	D	D	D
83	88		L	V	V	V
84	89		G	G	G	G
85	90		L	V	V	V
86	91		Y	Y	Y	Y
87	92		Y	Y	Y	Y
88	93		C	C	C	C
89	94	CDR3	W	W	M	M
90	95		Q	Q	Q	Q
91	96		G	G	A	A
92	97		T	T	L	L
93	98		H	H	Q	Q
94	99		F	F	T	T
95	100		P	P	P	P
96	101		R	R	R	
97	102		T	T	T	

98	103	FR4	F	F	F
99	104		G	G	G
100	105		G	Q	Q
101	106		G	G	G
102	107		T	T	T
103	108		K	K	K
104	109		L	V	V
105	110		E	E	E
106	111		I	I	I
106A	112		K	K	K

Table 14. Key to Kabat Numbering for Heavy Chain

KAB #	#	TYPE	Mouse 3D6 VH	HUM 3D6 VH	KABID 045919	VH3-23 Germ-line	Comment
1	1	FR1	E	E	E	E	
2	2		V	V	V	V	
3	3		K	Q	Q	Q	
4	4		L	L	L	L	
5	5		V	L	L	L	
6	6		E	E	E	E	
7	7		S	S	S	S	
8	8		G	G	G	G	
9	9		G	G	G	G	
10	10		G	G	G	G	
11	11		L	L	L	L	
12	12		V	V	V	V	
13	13		K	Q	Q	Q	
14	14		P	P	P	P	
15	15		G	G	G	G	
16	16		A	G	G	G	
17	17		S	S	S	S	
18	18		L	L	L	L	
19	19		K	R	R	R	
20	20		L	L	L	L	
21	21		S	S	S	S	
22	22		C	C	C	C	
23	23		A	A	A	A	
24	24		A	A	A	A	
25	25		S	S	S	S	
26	26		G	G	G	G	
27	27		F	F	F	F	
28	28		T	T	T	T	
29	29		F	F	F	F	
30	30		S	S	S	S	
31	31	CDR1	N	N	S	S	
32	32		Y	Y	Y	Y	
33	33		G	G	A	A	
34	34		M	M	V	M	
35	35		S	S	S	S	

36	36	FR2	W	W	W	W	
37	37		V	V	V	V	
38	38		R	R	R	R	
39	39		Q	Q	Q	Q	
40	40		N	A	A	A	Rare mouse, replace w/Hum
41	41		S	P	P	P	
42	42		D	G	G	G	Rare mouse, replace w/Hum
43	43		K	K	K	K	
44	44		R	G	G	G	
45	45		L	L	L	L	
46	46		E	E	E	E	
47	47		W	W	W	W	
48	48		V	V	V	V	
49	49		A	A	S	S	CDR contact/veneer
50	50	CDR2	S	S	A	A	
51	51		I	I	I	I	
52	52		R	R	S	S	
52A	53		S	S	G	G	
53	54		G	G	S	S	
54	55		G	G	G	G	
55	56		G	G	G	G	
56	57		R	R	S	S	
57	58		T	T	T	T	
58	59		Y	Y	Y	Y	
59	60		Y	Y	Y	Y	
60	61		S	S	A	A	
61	62		D	D	D	D	
62	63		N	N	S	S	
63	64		V	V	V	V	
64	65		K	K	K	K	
65	66		G	G	G	G	

66	67	FR3	R	R	R	R	
67	68		F	F	F	F	
68	69		T	T	T	T	
69	70		I	I	I	I	
70	71		S	S	S	S	
71	72		R	R	R	R	
72	73		E	D	D	D	
73	74		N	N	N	N	
74	75		A	A	A	S	
75	76		K	K	K	K	
76	77		N	N	N	N	
77	78		T	S	S	T	
78	79		L	L	L	L	
79	80		Y	Y	Y	Y	
80	81		L	L	L	L	
81	82		Q	Q	Q	Q	
82	83		M	M	M	M	
82A	84		S	N	N	N	
82B	85		S	S	S	S	
82C	86		L	L	L	L	
83	87		K	R	R	R	
84	88		S	A	A	A	
85	89		E	E	E	E	
86	90		D	D	D	D	
87	91		T	T	T	T	
88	92		A	A	A	A	
89	93		L	L	L	V	
90	94		Y	Y	Y	Y	
91	95		Y	Y	Y	Y	
92	96		C	C	C	C	
93	97		V	V	A	A	Packing residue, use mouse
94	98		R	R	K	K	Canonical, use mouse
95	99	CDR3	Y	Y	D		
96	100		D	D	N		
97	101		H	H	Y		
98	102		Y	Y	D		
99	103		S	S	F		
100	104		G	G	W		
100A	105		S	S	S		
100B	106		S	S	G		
100C	107		-	-	T		
100D	108		-	-	F		
101	109		D	D	D		
102	110		Y	Y	Y		

103	111	FR4	W	W	W
104	112		G	G	G
105	113		Q	Q	Q
106	114		G	G	G
107	115		T	T	T
108	116		T	L	L
109	117		V	V	V
110	118		T	T	T
111	119		V	V	V
112	120		S	S	S
113	121		S	S	S

The humanized antibodies preferably exhibit a specific binding affinity for Aβ of at least 10^7, 10^8, 10^9 or 10^{10} M^{-1}. Usually the upper limit of binding affinity of the humanized antibodies for Aβ is within a factor of three, four or five of that of 3D6 (*i.e.*, ~10^9 M^{-1}). Often the lower limit of binding affinity is also within a factor of three, four or five of that of 3D6.

Assembly and Expression of Humanized 3D6 VH and VL, Version 1
Briefly, for each V region, 4 large single stranded overlapping oligonucleotides were synthesized. In addition, 4 short PCR primers were synthesized for each V region to further facilitate assembly of the particular V region. The DNA sequences of the oligonucleotides employed for this purpose are shown in Table 15.

Table 15: DNA oligonucleotides

DNA#	SIZE	Coding?	Sequence	comments
4060	136	Yes	tccgc aagct tgccg ccacc ATGGA CATGC GCGTG CCCGC CCAGC TGCTG GGCCT GCTGA TGCTG TGGGT GTCCG GCTCC TCCGG CTACG TGGTG ATGAC CCAGT CCCCC CTGTC CCTGC CCGTG ACCCC CGGCG A (SEQ ID NO:17)	hum 3D6 VL-A
4061	131	No	CTGGG GGGAC TGGCC GGGCT TCTGC AGCAG CCAGT TCAGG TAGGT CTTGC CGTCG GAGTC CAGCA GGGAC TGGGA GGACT TGCAG GAGAT GGAGG CGGGC TCGCC GGGGG TCACG GGCAG GGACA GGGGG G (SEQ ID NO:18)	hum 3D6 VL-B
4062	146	Yes	ACCTG AACTG GCTGC TGCAG AAGCC CGGCC AGTCC CCCCA	hum 3D6 VL-C

			GCGCC TGATC TACCT GGTGT CCAAG CTGGA CTCCG GCGTG CCCGA CCGCT TCTCC GGCTC CGGCT CCGGC ACCGA CTTCA CCCTG AAGAT CTCCC GCGTG GAGGC C (SEQ ID NO:19)	
4063	142	No	aattc tagga tccac tcacg CTTGA TCTCC ACCTT GGTGC CCTGG CCGAA GGTGC GGGGG AAGTG GGTGC CCTGC CAGCA GTAGT ACACG CCCAC GTCCT CGGCC TCCAC GCGGG AGATC TTCAG GGTGA AGTCG GTGCC GG (SEQ ID NO:20)	hum 3D6 VL-D
4064	16	No	CTGGG GGGAC TGGCC G (SEQ ID NO: 21)	hum 3D6 VL A+B back %A+T = 18.75 [3]; % C+G = 81.2[13] Davis,Botstein,Roth Melting Temp C. 66.96
4065	22	Yes	ACCTG AACTG GCTGC TGCAG AA (SEQ ID NO:22)	hum 3D6 VL C+D forward % A+T = 45.45 [10]; % C+G = 54.55 [12] Davis,Botstein,Roth Melting Temp C. 64.54
4066	138	Yes	acaga aagct tgccg ccacc ATGGA GTTTG GGCTG AGCTG GCTTT TTCTT GTGGC TATTT TAAAA GGTGT CCAGT GTGAG GTGCA GCTGC TGGAG TCCGG CGGCG GCCTG GTGCA GCCCG GCGGC TCCCT GCGCC TGT (SEQ ID NO:23)	hum 3D6 VH-A
4067	135	No	GCCGC CGGAG CGGAT GGAGG CCACC CACTC CAGGC CCTTG CCGGG GGCCT GGCGC ACCCA GGACA TGCCG TAGTT GGAGA AGGTG AAGCC GGAGG CGGCG CAGGA CAGGC GCAGG GAGCC GCCGG GCTGC ACCAG (SEQ ID NO:24)	hum 3D6 VH-B
4068	142	Yes	CTGGA GTGGG TGGCC TCCAT CCGCT CCGGC GGCGG CCGCA CCTAC TACTC CGACA ACGTG AAGGG CCGCT TCACC ATCTC CCGCG ACAAC GCCAA GAACT CCCTG TACCT GCAGA TGAAC TCCCT GCGCG CCGAG GACAC CG (SEQ ID NO:25)	hum 3D6 VH-C
4069	144	No	ctgca aggat ccact caccG GAGGA CACGG TCACC AGGGT	hum 3D6 VH-D

			GCCCT GGCCC CAGTA GTCGG AGGAG CCGGA GTAGT GGTCG TAGCG CACGC AGTAG TACAG GGCGG TGTCC TCGGC GCGCA GGGAG TTCAT CTGCA GGTAC AGGG (SEQ ID NO:26)	
4070	16	No	GCCGC CGGAG CGGAT G (SEQ ID NO:27)	hum 3D6 VH A+B back % A+T = 18.75 [3]; % C+G = 81.25[13] Davis,Botstein,Roth Melting Temp C. 66.96
4071	20	Yes	CTGGA GTGGG TGGCC TCCAT (SEQ ID NO:28)	hum 3D6 VH C+D forward % A+T = 35.00 [7]; % C+G = 65.00 [13] Davis,Botstein,Roth Melting Temp C. 66.55
4072	19	Yes	tcc gca agc ttg ccg cca c (SEQ ID NO:29)	Hum 3D6 VL A+B Forward % A+T = 31.58 [6]; % C+G = 68.42[13] Davis,Botstein,Roth Melting Temp C. 66.64
4073	29	No	aat tct agg atc cac tca cgC TTG ATC TC (SEQ ID NO:30)	Hum 3D6 VL C+D Back % A+T = 55.17[16]; % C+G = 44.83 [13] Davis,Botstein,Roth Melting Temp C. 66.04
4074	23	Yes	aca gaa agc ttg ccg cca ccA TG (SEQ ID NO:31)	Hum 3D6 VH A+B Forward % A+T = 43.48 [10]; % C+G = 56.52 [13] Davis,Botstein,Roth Melting Temp C. 66.33
4075	22	No	ctg caa gga tcc act cac cGG A (SEQ ID NO:32)	Hum 3D6 VH C+D Back % A+T = 40.91 [9]; % C+G = 59.09[13] Davis,Botstein,Roth Melting Temp C. 66.40

The humanized light chain was assembled using PCR. DNA sequence analysis of greater than two dozen clones revealed scattered point mutations and

deletions throughout the VL region with respect to the expected sequence. Analysis of the sequences indicated that clone 2.3 was amenable to repair of 2 closely spaced single nucleotide deletions in the amino-terminal region. Hence site directed mutagenesis was performed on clone pCRShum3D6v12.3 using oligonucleotides to introduce the 2 deleted nucleotides, and repair of the point mutations was confirmed by DNA sequence analysis, and the VL insert was cloned into the light chain expression vector pCMV-cK.

Assembly of humanized VH using PCR-based methods resulted in clones with gross deletions in the 5' half of the sequence. Further efforts to optimize the PCR conditions met with partial success. The clones assembled via optimized PCR conditions still had 10-20 nt deletions in the region mapping to the overlap of the A+B fragments. Consequently, an alternate strategy was employed for VH assembly utilizing DNA polymerase (T4, Klenow, and Sequenase) mediated overlap extension, followed by T4 DNA ligase to covalently join the overlapping ends. DNA sequence analysis of a subset of the clones resulting from VH assembly using the latter approach revealed scattered point mutations and deletions among the clones. Analysis of over two dozen clones revealed essentially the same pattern as illustrated for the clones. The similar results observed following first pass assembly of VH and VL clones suggests the DNA sequence errors observed resulted from automated synthesizer errors during the synthesis of the long DNAs employed for the assembly.

Humanized VH clone 2.7 was selected for site-directed mutagenesis-mediated repair of the 3 nucleotide deletions it was observed to contain.

Example XIII: Characterization of Humanized 3D6v2 Antibody

A second version of humanized 3D6 was created having each of the substitutions indicated for version 1, except for the D→ Y substitution at residue 1. Substitution at this residue was performed in version 1 because the residue was identified as a CDR interacting residue. However, substitution deleted a residue which was rare for human immunoglobulins at that position. Hence, a version was created without the substitution. Moreover, non-germline residues in the heavy chain framework regions were substituted with germline residues, namely, H74 = S, H77 = T and H89 = V. Kabat numbering for the version 2 light and heavy chains, is the same as that depicted in Tables 13 and 14, respectively, except that residue 1 of the version 2 light chain is asp (D), residue 74 of the heavy chain is ser (S), residue 77 of the heavy

chain is thr (T) and residue 89 of the heavy chain is val (V). The nucleotide sequence of humanized 3D6 version 1 light and heavy chains are set forth as SEQ ID NOs: 34 and 36, respectively. The nucleotide sequence of humanized 3D6 version 2 light and heavy chains are set forth as SEQ ID NOs: 35 and 37, respectively.

Example IX: Functional Testing of Humanized 3D6 Antibodies

Binding of humanized 3D6v1 to aggregated Aβ. Functional testing of humanized 3D6v1 was conducted using conditioned media from transiently transfected COS cells. The cells were transfected with fully chimeric antibody, a mixture of either chimeric heavy chain + humanized light chain, or chimeric light chain + humanized heavy chain, and lastly, fully humanized antibody. The conditioned media was tested for binding to aggregated Aβ1-42 by ELISA assay. The humanized antibody showed good activity within experimental error, and displayed binding properties indistinguishable from the chimeric 3D6 reference sample. The results are shown in Table 16.

Table 16:

ng/ml	Chimeric	hu VH/ ChVL	ChVH/ HuVL	Hu VH/ HuVL
690			0.867	
600				0.895
260	0.83			
230			0.774	
200				0.81
190		0.811		
87	0.675			
77			0.594	
67				0.689
63		0.648		
29	0.45			
25			0.381	
22				0.496
21		0.438		
9.6	0.251			
8.5			0.198	
7.4				0.278
7		0.232		
3.2	0.129			
2.3		0.124		

To compare the binding affinities of humanized 3D6v1 and 3D6v2 antibodies, ELISA analysis was performed using aggregated Aβ as the antigen. The results show that both 3D6v1 (H1L1) and 3D6v2 (H2L2) have nearly identical Aβ binding properties (Figure 5).

Replacement NET (rNET) analysis of h3D6v2. The rNET epitope map assay provides information about the contribution of individual residues within the epitope to the overall binding activity of the antibody. rNET analysis uses synthesized systematic single substituted peptide analogs. Binding of an antibody being tested is determined against native peptide (native antigen) and against 19 alternative "single substituted" peptides, each peptide being substituted at a first position with one of 19 non-native amino acids for that position. A profile is generated reflecting the effect of substitution at that position with the various non-native residues. Profiles are likewise generated at successive positions along the antigenic peptide. The combined profile, or epitope map, (reflecting substitution at each position with all 19 non-native residues) can then be compared to a map similarly generated for a second antibody. Substantially similar or identical maps indicate that antibodies being compared have the same or similar epitope specificity.

This analysis was performed for 3D6 and humanized 3D6, version 2. Antibodies were tested for binding against the native Aβ peptide DAEFRHDSGY (SEQ ID NO:33). Residues 1-8 were systematically substituted with each of the 19 non-native residues for that position. Maps were generated accordingly for 3D6 and h3D6v2. The results are presented in tabular form in Table 17.

Table 17: Aβ: replacement Net Epitope (rNET) mapping of wt3D6 and humanized 3D6

Substitution	Wildtype 3D6 [OD]	Humanized 3D6 [OD]	Substitution	Wildtype 3D6 [OD]	Humanized 3D6 [OD]
Residue 1 = A	0.464	0.643	Residue 5 = A	0.275	0.435
C	0.450	0.628	C	0.359	0.635
D	**0.577**	**0.692**	D	0.080	0.163
E	0.576	0.700	E	0.115	0.187
F	0.034	0.062	F	0.439	0.569
G	0.569	0.738	G	0.485	0.679
H	0.054	0.117	H	0.577	0.680
I	0.048	0.118	I	0.510	0.671
K	0.033	0.057	K	0.573	0.693

	L	0.073	0.148		L	0.517	0.691
	M	0.039	0.072		M	0.418	0.611
	N	0.587	0.757		N	0.476	0.655
	P	0.069	0.144		P	0.093	0.198
	Q	0.441	0.689		Q	0.388	0.565
	R	0.056	0.155		**R**	**0.613**	**0.702**
	S	0.569	0.762		S	0.487	0.633
	T	0.450	0.702		T	0.530	0.639
	V	0.057	0.190		V	0.493	0.562
	W	0.031	0.070		W	0.393	0.461
	Y	0.341	0.498		Y	0.278	0.230
Residue 2 =	**A**	**0.548**	**0.698**	Residue 6 =	A	0.587	0.707
	C	0.553	0.694		C	0.585	0.703
	D	0.119	0.222		D	0.584	0.701
	E	0.563	0.702		E	0.579	0.702
	F	0.577	0.717		F	0.586	0.704
	G	0.527	0.720		G	0.592	0.709
	H	0.534	0.741		**H**	**0.596**	**0.688**
	I	0.522	0.722		I	0.602	0.708
	K	0.548	0.722		K	0.585	0.691
	L	0.482	0.705		L	0.584	0.688
	M	0.535	0.705		M	0.583	0.687
	N	0.525	0.735		N	0.580	0.686
	P	0.445	0.707		P	0.587	0.705
	Q	0.567	0.756		Q	0.570	0.695
	R	0.562	0.719		R	0.576	0.686
	S	0.587	0.705		S	0.573	0.689
	T	0.552	0.712		T	0.573	0.700
	V	0.550	0.702		V	0.588	0.715
	W	0.553	0.701		W	0.576	0.696
	Y	0.547	0.704		Y	0.595	0.708
Residue 3 =	A	0.038	0.061	Residue 7 =	A	0.580	0.688
	C	0.222	0.410		C	0.559	0.676
	D	0.019	0.027		**D**	**0.573**	**0.681**
	E	**0.542**	**0.689**		E	0.565	0.677
	F	0.034	0.060		F	0.546	0.668
	G	0.016	0.019		G	0.562	0.679
	H	0.016	0.020		H	0.557	0.675
	I	0.019	0.024		I	0.552	0.681
	K	0.053	0.090		K	0.565	0.685
	L	0.019	0.026		L	0.566	0.701
	M	0.019	0.027		M	0.562	0.697
	N	0.024	0.032		N	0.573	0.688
	P	0.017	0.020		P	0.582	0.678
	Q	0.153	0.406		Q	0.563	0.679
	R	0.015	0.023		R	0.551	0.677
	S	0.016	0.021		S	0.563	0.674
	T	0.015	0.019		T	0.560	0.685
	V	0.016	0.021		V	0.563	0.687
	W	0.149	0.304		W	0.547	0.685
	Y	0.016	0.020		Y	0.560	0.682

Residue 4 = A	0.016	0.020	Residue 8 = A	0.573	0.687
C	0.020	0.023	C	0.583	0.700
D	0.017	0.020	D	0.586	0.697
E	0.016	0.021	E	0.601	0.701
F	**0.557**	**0.703**	F	0.586	0.687
G	0.016	0.020	G	0.569	0.681
H	0.470	0.723	H	0.559	0.683
I	0.119	0.360	I	0.568	0.686
K	0.015	0.018	K	0.557	0.698
L	0.559	0.716	L	0.570	0.686
M	0.549	0.725	M	0.571	0.693
N	0.085	0.089	N	0.573	0.700
P	0.030	0.056	P	0.574	0.694
Q	0.065	0.110	Q	0.590	0.703
R	0.016	0.019	R	0.589	0.699
S	0.026	0.031	**S**	**0.599**	**0.719**
T	0.016	0.021	T	0.586	0.689
V	0.213	0.494	V	0.578	0.688
W	0.291	0.568	W	0.567	0.687
Y	0.529	0.730	Y	0.574	0.680

Notably, the profiles are virtually identical for 3D6 and h3D6v2 when one looks at the substitutions at each position (*i.e.*, the values fluctuate in an identical manner when comparing the data in column 1 (3D6) versus column 2 (h3D6v2). These data demonstrate that the specificity of h3D6v2 is preserved, as the h3D6v2 rNET epitope map is virtually identical to m3D6 using both Aβ residues 1-4 and 5-8.

Immunohistochemistry on PDAPP brain sections demonstrates specificity of h3D6v1 antibody. Humanized 3D6v1 antibody recognized Aβ in cryostat prepared brain sections from PDAPP mice. Humanized 3D6v1 and PK1614 both bound to PDAPP plaques in the same dose response fashion, as measured by the amount of fluorescence (quantitated in pixels) per slide versus the amount of antibody used to stain the tissue (Figure 6). Identical anti-human secondary antibodies were used in this experiment. Sectioning, staining, and image procedures were previously described. In identical experiments, image analysis of h3D6v2 staining on PDAPP and AD brain sections revealed that h3D6v2 recognizes Aβ plaques in a similar manner to 3D6v1 (*e.g.*, highly decorated plaques).

Competitive binding analysis of h3D6. The ability of h3D6 antibodies v1 and v2 to compete with murine 3D6 was measured by ELISA using a biotinylated 3D6 antibody. Competitive binding analysis revealed that h3D6v1, h3D6v2, and chimeric

PK1614 can all compete with m3D6 to bind Aβ (Figure 7). h3D6v1 and h3D6v2 were identical in their ability to compete with 3D6 to Aβ. The 10D5 antibody was used as a negative control, as it has a different binding epitope than 3D6. BIAcore analysis also revealed a high affinity of h3D6v1 and h3D6v2 for Aβ (Table 18).

Table 18: Affinity Measurements of Aβ Antibodies Using BIAcore Technology

Antibody	**ka1 (1/Ms)**	**kd1 (1/s)**	**Kd (nM)**
Mu 3D6	4.06E +05	3.57E-04	0.88
Chimeric 3D6	4.58E+05	3.86E-04	0.84
Hu 3D6v1	1.85E+05	3.82E-04	2.06
Hu 3D6v2	1.70E+05	3.78E-04	2.24

In comparison to 3D6, which has a Kd of 0.88 nM, both h3D6v1 and h3D6v2 had about a 2 to 3 fold less binding affinity, measured at 2.06 nM and 2.24 nM for h3D6v1 and h3D6v2, respectively. The ELISA competitive binding assay revealed an approximate 6-fold less binding affinity for h3D6v1 and h3D6v2. Typically humanized antibodies lose about 3-4 fold in binding affinity in comparison to their murine counterparts. Therefore, a loss of about 3 fold (average of ELISA and BIAcore results) for h3D6v1 and h3D6v2 is within the accepted range.

Ex vivo assay using h3D6v2 antibody. The ability of h3D6v2 to stimulate microglial cells was tested through an *ex vivo* phagocytosis assay (Figure 8). h3D6v2 was as effective as chimeric 3D6 at inducing phagocytosis of Aβ aggregates from PDAPP mouse brain tissue. IgG was used as a negative control in this experiment because it is incapable of binding Aβ and therefore cannot induce phagocytosis.

In vivo brain localization of h3D6. ^{125}I labeled h3D6v2, m3D6, and antibody DAE13 were each IV-injected into 14 individual PDAPP mice in separate experiments. Mice were sacrificed after Day 7 and perfused for further analysis. Their brain regions were dissected and measured for ^{125}I activity in specific brain regions. Radiolabel activity in the brain was compared with activity in serum samples. Results are set forth in Tables 19 and 20, for serum and brain regions, respectively.

Table 19

m3D6	DAE13	Hu3D6
30389.1	17463.9	40963.8
12171	13200.6	24202.2
3418.2	36284.7	12472.4
18678.9	421.3	33851.8
27241	19702	27187.3
26398.8	24855.8	29016.9
27924.8	29287.4	33830.7
12008.4	12733.1	26734.9
29487.8	27722.5	30144.5
25498.6	30460.7	35126.9
9652	23320.1	28414.8
24599.3	7119.1	16956.1
29240	28093.5	18190.7
11922.7	24659.7	25671.4
17443.1	26748.9	

Table 20

m3D6			DAE13			Hu3D6 (H2L2)		
cere	cort	hipp	cere	cort	hipp	cere	cort	hipp
1991.9	1201.1	4024	1277.5	2522.9	5711.9	2424.6	3759.4	11622
238.9	746.1	2523	502.5	2123.5	6965.8	1509.8	2274.9	7018.2
645.9	603	1241.1	2325	3528.2	7801.6	500	2265.9	5316.3
1000	2508.2	4644.2	232.7	849.8	1891.9	2736.2	5703.7	10395.5
1266.9	3737.9	7975.8	891.6	2621	8245.2	1192.2	3188	10170
1422	2398.7	7731.1	1102.6	2087.5	7292.3	2269.4	3481.4	9621.6
1700.4	2154.4	7124.1	1650.6	3488.4	10284.8	1526.7	3028	8331.3
542.5	812.4	2456.8	712.9	2318.5	6643.3	1538.1	4194.1	11244.8
1309	3010.5	8693.5	1172.9	1953.6	7363	1245.7	1699.4	6831.2
1372.2	997.5	2425.4	1067.9	3697.2	12280.7	2708.8	2789	7887.4
778.6	1291.9	5654.4	1952.2	2120.7	6412.7	2251.3	3897.5	11121.5
1199.3	1683.4	4887.3	1005.2	1852.5	5121.4	1529.6	1772.2	7986.9
1021.8	3234.5	8036.2	961.5	3382.9	8473.1	644.1	1663.4	5056.5
742.1	1056.7	3405.2	852.3	1943.2	6717.4	1516.4	1620.6	9888
1273.7	1320.8	4262.6	997.5	3065.7	10213.1			

The data show that h3D6v2 localized to the brain, and was particularly concentrated in the hippocampal region where Aβ is known to aggregate. Brain counts for m3D6 and DAE13 were comparable to h3D6v2. All three antibodies were able to cross the blood barrier as demonstrated by Aβ plaque binding *in vivo*.

Example X. Cloning and Sequencing of the Mouse 10D5 Variable Regions

Cloning and Sequence Analysis of 10D5 VH. The VH and VL regions of 10D5 from hybridoma cells were cloned by RT-PCR using 5' RACE procedures. The nucleotide sequence (SEQ ID NO:13) and deduced amino acid sequence (SEQ ID NO:14) derived from two independent cDNA clones encoding the presumed 10D5 VL

domain, are set forth in Table 21 and Figure 9. The nucleotide sequence (SEQ ID NO:15) and deduced amino acid sequence (SEQ ID NO:16) derived from two independent cDNA clones encoding the presumed 10D5 VH domain, are set forth in Table 22 and Figure 10. The 10D5 VL and VH sequences meet the criteria for functional V regions in so far as they contain a contiguous ORF from the initiator methionine to the C-region, and share conserved residues characteristic of immunoglobulin V region genes.

Table 21: Mouse 10D5 VL DNA sequence

ATGAAGTTGCCTGTTAGGCTGTTGGTACTGATGTTCTGGATTCCTGCTTCCAGCAGTGA
TGTTTTGATGACCCAAACTCCACTCTCCCTGCCTGTCAGTCTTGGAGATCAAGCCTCCA
TCTCTTGCAGATCTAGTCAGAACATTATACATAGTAATGGAAACACCTATTTAGAATGG
TACCTGCAGAAACCAGGCCAGTCTCCAAAGCTCCTGATCTACAAAGTTTCCAACCGATT
TTCTGGGGTCCCAGACAGGTTCAGTGGCAGTGGATCAGGGACAGATTTCACACTCAAGA
TCAAGAAAGTGGAGGCTGAGGATCTGGGAATTTATTACTGCTTTCAAGGTTCACATGTT
CCGCTCACGTTCGGTGCTGGGACCAAGCTGGAGCTGGAA (SEQ ID NO:13)

*Leader peptide underlined

Table 22: Mouse 10D5 VH DNA sequence.

ATGGACAGGCTTACTTCCTCATTCCTGCTGCTGATTGTCCCTGCATATGTCCTGTCCCA
GGCTACTCTGAAAGAGTCTGGCCCTGGAATATTGCAGTCCTCCCAGACCCTCAGTCTGA
CTTGTTCTTTCTCTGGGTTTTCACTGAGCACTTCTGGTATGGGAGTGAGCTGGATTCGT
CAGCCTTCAGGAAAGGGTCTGGAGTGGCTGGCACACATTTACTGGGATGATGACAAGCG
CTATAACCCATCCCTGAAGAGCCGGCTCACAATCTCCAAGGATACCTCCAGAAAGCAGG
TATTCCTCAAGATCACCAGTGTGGACCCTGCAGATACTGCCACATACTACTGTGTTCGA
AGGCCCATTACTCCGGTACTAGTCGATGCTATGGACTACTGGGGTCAAGGAACCTCAGT
CACCGTCTCCTCA (SEQ ID NO:15)

*Leader peptide underlined.

Example XI: Efficacy of mAb 3D6 on various neuropathological endpoints in PDAPP mice

This Example describes the efficacy of murine mAb 3D6 on various neuropathological endpoints. A comparison is made between passive immunization with 3D6 (at varying doses) and active immunization with an Aβ peptide.

Immunizations

PDAPP mice were passively immunized with mAb 3D6 at three different doses, 10 mg/kg, 1 mg/kg and 10 mg/kg once a month (1 x 4). An unrelated IgGγ2a antibody (TY 11/15) and PBS injections served as controls. Active immunization with Aβ peptide served as a comparison. Between 20 and 35 animals were analyzed in each group.

The neuropathological endpoints assayed include amyloid burden and neuritic burden.

Amyloid burden

The extent of the frontal cortex occupied by amyloid deposits was determined by immunostaining with 3D6 followed by quantitative image analysis. The results of this analysis are shown in Table 6. Each of the immunotherapies led to a significant reduction of amyloid burden.

Neuritic burden

Neuritic burden following passive immunization with 3D6 was determined in PDAPP mice by immunostaining of brain sections with anti-APP antibody 8E5 followed by quantitative image analysis. Neuritic dystrophy is indicated by the appearance of dystrophic neurites (*e.g.*, neurites with a globular appearance) located in the immediate vicinity of amyloid plaques. The results of this analysis are shown in Table 7. 3D6 (IgGγ2a isotype, recognizing Aβ 1-5) did not significantly reduce neuritic burden as compared to active immunization with Aβ peptide. Previously, it had been observed that 10D5 (IgGγ1 isotype recognizing Aβ 3-7) was unable to significantly reduce neuritic burden.

Table 23: Frontal Cortex Amyloid Burden

	PBS	TY 11/15	3D6, 10 mg/kg	3D6, 1 mg/kg	3D6, 10 mg/kg/4 wks.	Active
N	31	30	29	31	32	24
Median (%AB)	15.182297	13.303288	0.865671	2.286513	1.470956	2.162772
Range	0.160-31.961	0-61.706	0-7.064	0.077-63.362	0-10.688	0-30.715
p Value (*M-W)		.9425 ns	***.0001	*** <.0001	*** <.0001	***.0004
% Change	N/A	12%	94%	85%	90%	86%

Table 24: Frontal Cortex Neuritic Burden

	PBS	TY 11/15	3D6, 10 mg/kg	3D6, 1 mg/kg	3D6, 10 mg/kg/4 wks.	Active
N	31	30	29	31	32	24
Median (%NB)	0.3946	0.3958	0.4681	0.3649	0.4228	0.2344
Range	0-1.3828	0-2.6800	0-1.3098	0-1.5760	0-1.8215	0-1.1942
p Value (*M-W)		.8967 ns	.9587 ns	.6986 ns	>.9999	***.0381
% Change		0%	0%	7%	0%	41%

The characterization of various neuropathological endpoints in the PDAPP mouse model of Alzheimer's disease may assist the skilled artisan in designing appropriate human therapeutic immunization protocols.

Example XII. Prevention and Treatment of Human Subjects

A single-dose phase I trial is performed to determine safety in humans. A therapeutic agent is administered in increasing dosages to different patients starting from about 0.01 the level of presumed efficacy, and increasing by a factor of three until a level of about 10 times the effective mouse dosage is reached.

A phase II trial is performed to determine therapeutic efficacy. Patients with early to mid Alzheimer's Disease defined using Alzheimer's disease and Related Disorders Association (ADRDA) criteria for probable AD are selected. Suitable patients score in the 12-26 range on the Mini-Mental State Exam (MMSE). Other selection criteria are that patients are likely to survive the duration of the study and lack complicating issues such as use of concomitant medications that may interfere. Baseline evaluations of patient function are made using classic psychometric measures, such as the MMSE, and the ADAS, which is a comprehensive scale for evaluating patients with Alzheimer's Disease status and function. These psychometric scales provide a measure of progression of the Alzheimer's condition. Suitable qualitative life scales can also be used to monitor treatment. Disease progression can also be monitored by MRI. Blood profiles of patients can also be monitored including assays of immunogen-specific antibodies and T-cells responses.

Following baseline measures, patients begin receiving treatment. They are randomized and treated with either therapeutic agent or placebo in a blinded fashion. Patients are monitored at least every six months. Efficacy is determined by a significant reduction in progression of a treatment group relative to a placebo group.

A second phase II trial is performed to evaluate conversion of patients from non-Alzheimer's Disease early memory loss, sometimes referred to as age-associated memory impairment (AAMI) or mild cognitive impairment (MCI), to probable Alzheimer's disease as defined as by ADRDA criteria. Patients with high risk for conversion to Alzheimer's Disease are selected from a non-clinical population by screening reference populations for early signs of memory loss or other difficulties associated with pre-Alzheimer's symptomatology, a family history of Alzheimer's

Disease, genetic risk factors, age, sex, and other features found to predict high-risk for Alzheimer's Disease. Baseline scores on suitable metrics including the MMSE and the ADAS together with other metrics designed to evaluate a more normal population are collected. These patient populations are divided into suitable groups with placebo comparison against dosing alternatives with the agent. These patient populations are followed at intervals of about six months, and the endpoint for each patient is whether or not he or she converts to probable Alzheimer's Disease as defined by ADRDA criteria at the end of the observation.

General Materials and Methods

A. Preparation of Polyclonal and Monoclonal Aβ Antibodies

The anti-Aβ polyclonal antibody was prepared from blood collected from two groups of animals. The first group consisted of 100 female Swiss Webster mice, 6 to 8 weeks of age. They were immunized on days 0, 15, and 29 with 100 μg of AN1792 combined with CFA/IFA. A fourth injection was given on day 36 with one-half the dose of AN1792. Animals were exsanguinated upon sacrifice at day 42, serum was prepared and the sera were pooled to create a total of 64 ml. The second group consisted of 24 female mice isogenic with the PDAPP mice but nontransgenic for the human APP gene, 6 to 9 weeks of age. They were immunized on days 0, 14, 28 and 56 with 100 μg of AN1792 combined with CFA/IFA. These animals were also exsanguinated upon sacrifice at day 63, serum was prepared and pooled for a total of 14 ml. The two lots of sera were pooled. The antibody fraction was purified using two sequential rounds of precipitation with 50% saturated ammonium sulfate. The final precipitate was dialyzed against PBS and tested for endotoxin. The level of endotoxin was less than 1 EU/mg.

The anti-Aβ monoclonal antibodies were prepared from ascites fluid. The fluid was first delipidated by the addition of concentrated sodium dextran sulfate to ice-cold ascites fluid by stirring on ice to a reach a final concentration of 0.238%. Concentrated $CaCl_2$ was then added with stirring to reach a final concentration of 64mM. This solution was centrifuged at 10,000 x g and the pellet was discarded. The supernatant was stirred on ice with an equal volume of saturated ammonium sulfate added dropwise. The solution was centrifuged again at 10,000 x g and the supernatant was discarded. The pellet was resuspended and dialyzed against 20 mM Tris-HCl , 0.4

M NaCl, pH 7.5. This fraction was applied to a Pharmacia FPLC Sepharose Q Column and eluted with a reverse gradient from 0.4 M to 0.275 M NaCl in 20 mM Tris-HCl, pH 7.5.

The antibody peak was identified by absorbance at 280 nm and appropriate fractions were pooled. The purified antibody preparation was characterized by measuring the protein concentration using the BCA method and the purity using SDS-PAGE. The pool was also tested for endotoxin. The level of endotoxin was less than 1 EU/mg. titers, titers less than 100 were arbitrarily assigned a titer value of 25.

B. Measurement of Antibody Titers

Mice were bled by making a small nick in the tail vein and collecting about 200 μl of blood into a microfuge tube. Guinea pigs were bled by first shaving the back hock area and then using an 18 gauge needle to nick the metatarsal vein and collecting the blood into microfuge tubes. Blood was allowed to clot for one hr at room temperature (RT), vortexed, then centrifuged at 14,000 x g for 10 min to separate the clot from the serum. Serum was then transferred to a clean microfuge tube and stored at 4°C until titered.

Antibody titers were measured by ELISA. 96-well microtiter plates (Costar EIA plates) were coated with 100 μl of a solution containing either 10 μg/ml either Aβ42 or SAPP or other antigens as noted in each of the individual reports in Well Coating Buffer (0.1 M sodium phosphate, pH 8.5, 0.1% sodium azide) and held overnight at RT. The wells were aspirated and sera were added to the wells starting at a 1/100 dilution in Specimen Diluent (0.014 M sodium phosphate, pH 7.4, 0.15 M NaCl, 0.6% bovine serum albumin, 0.05% thimerosal). Seven serial dilutions of the samples were made directly in the plates in three-fold steps to reach a final dilution of 1/218,700. The dilutions were incubated in the coated-plate wells for one hr at RT. The plates were then washed four times with PBS containing 0.05% Tween 20. The second antibody, a goat anti-mouse Ig conjugated to horseradish peroxidase (obtained from Boehringer Mannheim), was added to the wells as 100 μl of a 1/3000 dilution in Specimen Diluent and incubated for one hr at RT. Plates were again washed four times in PBS, Tween 20. To develop the chromogen, 100 μl of Slow TMB (3,3',5,5'-tetramethyl benzidine obtained from Pierce Chemicals) was added to each well and incubated for 15 min at

RT. The reaction was stopped by the addition of 25 µl of 2 M H_2SO_4. The color intensity was then read on a Molecular Devices Vmax at (450 nm - 650 nm).

Titers were defined as the reciprocal of the dilution of serum giving one half the maximum OD. Maximal OD was generally taken from an initial 1/100 dilution, except in cases with very high titers, in which case a higher initial dilution was necessary to establish the maximal OD. If the 50% point fell between two dilutions, a linear extrapolation was made to calculate the final titer. To calculate geometric mean antibody titers, titers less than 100 were arbitrarily assigned a titer value of 25.

C. Brain Tissue Preparation

After euthanasia, the brains were removed and one hemisphere was prepared for immunohistochemical analysis, while three brain regions (hippocampus, cortex and cerebellum) were dissected from the other hemisphere and used to measure the concentration of various Aβ proteins and APP forms using specific ELISAs (Johnson-Wood *et al.*, *supra*).

Tissues destined for ELISAs were homogenized in 10 volumes of ice-cold guanidine buffer (5.0 M guanidine-HCl, 50 mM Tris-HCl, pH 8.0). The homogenates were mixed by gentle agitation using an Adams Nutator (Fisher) for three to four hr at RT, then stored at -20°C prior to quantitation of Aβ and APP. Previous experiments had shown that the analytes were stable under this storage condition, and that synthetic Aβ protein (Bachem) could be quantitatively recovered when spiked into homogenates of control brain tissue from mouse littermates (Johnson-Wood *et al.*, *supra*).

D. Measurement of Aβ Levels

The brain homogenates were diluted 1:10 with ice cold Casein Diluent (0.25% casein, PBS, 0.05% sodium azide, 20 µg/ml aprotinin, 5 mM EDTA pH 8.0, 10 µg/ml leupeptin) and then centrifuged at 16,000 x g for 20 min at 4° C. The synthetic Aβ protein standards (1-42 amino acids) and the APP standards were prepared to include 0.5 M guanidine and 0.1% bovine serum albumin (BSA) in the final composition. The "total" Aβ sandwich ELISA utilizes monoclonal antibody monoclonal antibody 266, specific for amino acids 13-28 of Aβ (Seubert *et al.*, *supra*), as the capture antibody, and

biotinylated monoclonal antibody 3D6, specific for amino acids 1-5 of Aβ (Johnson-Wood *et al., supra*), as the reporter antibody. The 3D6 monoclonal antibody does not recognize secreted APP or full-length APP, but detects only Aβ species with an amino-terminal aspartic acid. This assay has a lower limit of sensitivity of ~50 ng/ml (11nM) and shows no cross-reactivity to the endogenous murine Aβ protein at concentrations up to 1 ng/ml (Johnson-Wood *et al., supra*).

The Aβ1-42 specific sandwich ELISA employs mAβ 21F12, specific for amino acids 33-42 of Aβ (Johnson-Wood, *et al. supra*), as the capture antibody. Biotinylated mAβ 3D6 is also the reporter antibody in this assay which has a lower limit of sensitivity of about 125 μg/ml (28 μM, Johnson-Wood *et al., supra*). For the Aβ ELISAs, 100 μl of either mAβ 266 (at 10 μg/ml) or mAβ 21F12 at (5 μg/ml) was coated into the wells of 96-well immunoassay plates (Costar) by overnight incubation at RT. The solution was removed by aspiration and the wells were blocked by the addition of 200 μl of 0.25% human serum albumin in PBS buffer for at least 1 hr at RT. Blocking solution was removed and the plates were stored desiccated at 4°C until used. The plates were rehydrated with Wash Buffer [Tris-buffered saline (0.15 M NaCl, 0.01 M Tris-HCl, pH 7.5), plus 0.05% Tween 20] prior to use. The samples and standards were added in triplicate aliquots of 100 μl per well and then incubated overnight at 4° C. The plates were washed at least three times with Wash Buffer between each step of the assay. The biotinylated mAβ 3D6, diluted to 0.5 μg/ml in Casein Assay Buffer (0.25% casein, PBS, 0.05% Tween 20, pH 7.4), was added and incubated in the wells for 1 hr at RT. An avidin-horseradish peroxidase conjugate, (Avidin-HRP obtained from Vector, Burlingame, CA), diluted 1:4000 in Casein Assay Buffer, was added to the wells for 1 hr at RT. The colorimetric substrate, Slow TMB-ELISA (Pierce), was added and allowed to react for 15 minutes at RT, after which the enzymatic reaction was stopped by the addition of 25 μl 2 N H2SO4. The reaction product was quantified using a Molecular Devices Vmax measuring the difference in absorbance at 450 nm and 650 nm.

E. Measurement of APP Levels

Two different APP assays were utilized. The first, designated APP-α/FL, recognizes both APP-alpha (α) and full-length (FL) forms of APP. The second assay is

specific for APP-α. The APP-α /FL assay recognizes secreted APP including the first 12 amino acids of Aβ. Since the reporter antibody (2H3) is not specific to the α-clip-site, occurring between amino acids 612-613 of APP^{695} (Esch *et al.*, Science 248:1122-1124 (1990)); this assay also recognizes full length APP (APP-FL). Preliminary experiments using immobilized APP antibodies to the cytoplasmic tail of APP-FL to deplete brain homogenates of APP-FL suggest that approximately 30-40% of the APP-α /FL APP is FL (data not shown). The capture antibody for both the APP-α/FL and APP-α assays is mAb 8E5, raised against amino acids 444 to 592 of the APP^{695} form (Games *et al.*, *supra*). The reporter mAb for the APP-α/FL assay is mAb 2H3, specific for amino acids 597-608 of APP^{695} (Johnson-Wood *et al.*, *supra*) and the reporter antibody for the APP-α assay is a biotinylated derivative of mAb 16H9, raised to amino acids 605 to 611 of APP. The lower limit of sensitivity of the APP-αFL assay is about 11 ng/ml (150 ρM) (Johnson-Wood *et al.*) and that of the APP-α specific assay is 22 ng/ml (0.3 nM). For both APP assays, mAb 8E5 was coated onto the wells of 96-well EIA plates as described above for mAb 266. Purified, recombinant secreted APP-α was used as the reference standard for the APP-α assay and the APP-α/FL assay (Esch *et al.*, *supra*). The brain homogenate samples in 5 M guanidine were diluted 1:10 in ELISA Specimen Diluent (0.014 M phosphate buffer, pH 7.4, 0.6% bovine serum albumin, 0.05% thimerosal, 0.5 M NaCl, 0.1% NP40). They were then diluted 1:4 in Specimen Diluent containing 0.5 M guanidine. Diluted homogenates were then centrifuged at 16,000 x g for 15 seconds at RT. The APP standards and samples were added to the plate in duplicate aliquots and incubated for 1.5 hr at RT. The biotinylated reporter antibody 2H3 or 16H9 was incubated with samples for 1 hr at RT. Streptavidin-alkaline phosphatase (Boehringer Mannheim), diluted 1:1000 in specimen diluent, was incubated in the wells for 1 hr at RT. The fluorescent substrate 4-methyl-umbellipheryl-phosphate was added for a 30-min RT incubation and the plates were read on a Cytofluor tm 2350 fluorimeter (Millipore) at 365 nm excitation and 450 nm emission.

F. Immunohistochemistry

Brains were fixed for three days at 40C in 4% paraformaldehyde in PBS and then stored from one to seven days at 4°C in 1% paraformaldehyde, PBS until sectioned. Forty-micron-thick coronal sections were cut on a vibratome at RT and

stored in cryoprotectant (30% glycerol, 30% ethylene glycol in phosphate buffer) at -20°C prior to immunohistochemical processing. For each brain, six sections at the level of the dorsal hippocampus, each separated by consecutive 240 μm intervals, were incubated overnight with one of the following antibodies: (1) a biotinylated anti-Aβ (mAb, 3D6, specific for human Aβ) diluted to a concentration of 2 μg/ml in PBS and 1% horse serum; or (2) a biotinylated mAb specific for human APP, 8E5, diluted to a concentration of 3 μg/ml in PBS and 1.0% horse serum; or (3) a mAb specific for glial fibrillary acidic protein (GFAP; Sigma Chemical Co.) diluted 1:500 with 0.25% Triton X-100 and 1% horse serum, in Tris-buffered saline, pH 7.4 (TBS); or (4) a mAb specific for CD11b, MAC-1 antigen, (Chemicon International) diluted 1:100 with 0.25% Triton X-100 and 1% rabbit serum in TBS; or (5) a mAb specific for MHC II antigen, (Pharmingen) diluted 1:100 with 0.25% Triton X-100 and 1% rabbit serum in TBS; or (6) a rat mAb specific for CD 43 (Pharmingen) diluted 1:100 with 1% rabbit serum in PBS or (7) a rat mAb specific for CD 45RA (Pharmingen) diluted 1:100 with 1% rabbit serum in PBS; or (8) a rat monoclonal Aβ specific for CD 45RB (Pharmingen) diluted 1:100 with 1% rabbit serum in PBS; or (9) a rat monoclonal Aβ specific for CD 45 (Pharmingen) diluted 1:100 with 1% rabbit serum in PBS; or (10) a biotinylated polyclonal hamster Aβ specific for CD3e (Pharmingen) diluted 1:100 with 1% rabbit serum in PBS or (11) a rat mAb specific for CD3 (Serotec) diluted 1:200 with 1% rabbit serum in PBS; or with (12) a solution of PBS lacking a primary antibody containing 1% normal horse serum.

Sections reacted with antibody solutions listed in 1,2 and 6-12 above were pretreated with 1.0% Triton X-100, 0.4% hydrogen peroxide in PBS for 20 min at RT to block endogenous peroxidase. They were next incubated overnight at 4°C with primary antibody. Sections reacted with 3D6 or 8E5 or CD3e mAbs were then reacted for one hr at RT with a horseradish peroxidase-avidin-biotin-complex with kit components "A" and "B" diluted 1:75 in PBS (Vector Elite Standard Kit, Vector Labs, Burlingame, CA.). Sections reacted with antibodies specific for CD 45RA, CD 45RB, CD 45, CD3 and the PBS solution devoid of primary antibody were incubated for 1 hour at RT with biotinylated anti-rat IgG (Vector) diluted 1:75 in PBS or biotinylated anti-mouse IgG (Vector) diluted 1:75 in PBS, respectively. Sections were then reacted for one hr at RT with a horseradish peroxidase-avidin-biotin-complex with kit components

"A" and "B" diluted 1:75 in PBS (Vector Elite Standard Kit, Vector Labs, Burlingame, CA.).

Sections were developed in 0.01% hydrogen peroxide, 0.05% 3,3'-diaminobenzidine (DAB) at RT. Sections destined for incubation with the GFAP-, MAC-1- AND MHC II-specific antibodies were pretreated with 0.6% hydrogen peroxide at RT to block endogenous peroxidase then incubated overnight with the primary antibody at 4°C. Sections reacted with the GFAP antibody were incubated for 1 hr at RT with biotinylated anti-mouse IgG made in horse (Vector Laboratories; Vectastain Elite ABC Kit) diluted 1:200 with TBS. The sections were next reacted for one hr with an avidin-biotin-peroxidase complex (Vector Laboratories; Vectastain Elite ABC Kit) diluted 1:1000 with TBS. Sections incubated with the MAC-1-or MHC II-specific monoclonal antibody as the primary antibody were subsequently reacted for 1 hr at RT with biotinylated anti-rat IgG made in rabbit diluted 1:200 with TBS, followed by incubation for one hr with avidin-biotin-peroxidase complex diluted 1:1000 with TBS. Sections incubated with GFAP-, MAC-1- and MHC II-specific antibodies were then visualized by treatment at RT with 0.05% DAB, 0.01% hydrogen peroxide, 0.04% nickel chloride, TBS for 4 and 11 min, respectively.

Immunolabeled sections were mounted on glass slides (VWR, Superfrost slides), air dried overnight, dipped in Propar (Anatech) and overlaid with coverslips using Permount (Fisher) as the mounting medium.

To counterstain Aβ plaques, a subset of the GFAP-positive sections were mounted on Superfrost slides and incubated in aqueous 1% Thioflavin S (Sigma) for 7 min following immunohistochemical processing. Sections were then dehydrated and cleared in Propar, then overlaid with coverslips mounted with Permount.

G. Image Analysis

A Videometric 150 Image Analysis System (Oncor, Inc., Gaithersburg, MD) linked to a Nikon Microphot-FX microscope through a CCD video camera and a Sony Trinitron monitor was used for quantification of the immunoreactive slides. The image of the section was stored in a video buffer and a color-and saturation-based threshold was determined to select and calculate the total pixel area occupied by the immunolabeled structures. For each section, the hippocampus was manually outlined and the total pixel area occupied by the hippocampus was calculated. The percent

amyloid burden was measured as: (the fraction of the hippocampal area containing Aβ deposits immunoreactive with mAb 3D6) x 100. Similarly, the percent neuritic burden was measured as: (the fraction of the hippocampal area containing dystrophic neurites reactive with monoclonal antibody 8E5) x100. The C-Imaging System (Compix, Inc., Cranberry Township, PA) operating the Simple 32 Software Application program was linked to a Nikon Microphot-FX microscope through an Optronics camera and used to quantitate the percentage of the retrospenial cortex occupied by GFAP-positive astrocytes and MAC-1-and MHC II-positive microglia. The image of the immunoreacted section was stored in a video buffer and a monochrome-based threshold was determined to select and calculate the total pixel area occupied by immunolabeled cells. For each section, the retrosplenial cortex (RSC) was manually outlined and the total pixel area occupied by the RSC was calculated. The percent astrocytosis was defined as: (the fraction of RSC occupied by GFAP-reactive astrocytes) X 100. Similarly, percent microgliosis was defined as: (the fraction of the RSC occupied by MAC-1- or MHC II-reactive microglia) X 100. For all image analyses, six sections at the level of the dorsal hippocampus, each separated by consecutive 240 μm intervals, were quantitated for each animal. In all cases, the treatment status of the animals was unknown to the observer.

Although the foregoing invention has been described in detail for purposes of clarity of understanding, it will be obvious that certain modifications may be practiced within the scope of the appended claims. All publications and patent documents cited herein, as well as text appearing in the figures and sequence listing, are hereby incorporated by reference in their entirety for all purposes to the same extent as if each were so individually denoted.

From the foregoing it will be apparent that the invention provides for a number of uses. For example, the invention provides for the use of any of the antibodies to Aβ described above in the treatment, prophylaxis or diagnosis of amyloidogenic disease, or in the manufacture of a medicament or diagnostic composition for use in the same.